SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 1 of 21

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rag.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rag.

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OM protein - protein search, using sw model

Run on: December 14, 2010, 11:22:17; Search time 37 Seconds

(without alignments)

5898.160 Million cell updates/sec

Title: US-09-556-178-5 Perfect score: 882

Sequence: 1 MEALILEPSLYTVKAILILD......QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

564.5

564.5

64.0

Searched:

6395994 segs, 1224146475 residues

Total number of hits satisfying chosen parameters: 6395994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

3: geneseqp3:*

Database: A_Geneseq_201023:*
1: geneseqp1:*
2: geneseqp2:*

SUMMARIES

64.0 160 1 ABB60295

160 2 AFB87634

					SOMMANIES	
		8				
Result		Query				
No.	Score	Match	Length	DB	ID	Description
1	882	100.0	177	1	AAY49960	Aay49960 Human ves
2	882	100.0	177	1	AAB03815	Aab03815 Human ves
3	882	100.0	177	1	AAB03789	Aab03789 Human cap
4	882	100.0	177	1	ADO23737	Ado23737 COPI coat
5	882	100.0	177	2	AEJ65021	Aej65021 Liver can
6	882	100.0	177	3	AYI11804	Ayi11804 Human coa
7	845	95.8	177	1	AD057263	Ado57263 Kidney de
8	673	76.3	210	1	AAY31641	Aay31641 Human tra
9	673	76.3	210	1	ADO23725	Ado23725 COPI coat
10	673	76.3	210	3	AYI11805	Ayill805 Human coa
11	671	76.1	137	1	AAG01470	Aag01470 Human sec
1.2	580	65.8	185	1	ano21857	Ado21857 Human tree

Abb60295 Drosophil

Afb87634 Fruit flv

15	507.5	57.5	181	2	ARO36046	Aro36046	Soybean c
16	507.5	57.5	181	2	AR037763	Aro37763	Soybean c
17	507.5	57.5	181	3	AXJ10909	Axj10909	Heteroder
18	507.5	57.5	181	3	AXJ09192	Axj09192	Heteroder
19	493.5	56.0	175	2	ADY65214		S. manson
20	441.5	50.1	154	2	ARO39451	Aro39451	Soybean c
21	441.5	50.1	154	3	AXJ12597	Axj12597	Heteroder
22	440	49.9	99	1	AAB54324	Aab54324	Human pan
23	394	44.7	179	2	AFQ47080		Glycine m
24	386	43.8	177	2	ARM90905	Arm90905	Arabidops
25	386	43.8	177	2	ARM94661		Arabidops
26	379	43.0	177	2	ARB02835		Cotton pr
27	375.5	42.6	180	1	AFP84367		Glycine m
28	373	42.3	182	2	ARL84894		Maize pla
29	371	42.1	182	1	AAG35416		Zea mays
30	371	42.1	182	2	ALJ76006		Plant pro
31	371	42.1	182	2	AFC59274		Maize ami
32	371	42.1	182	2	ARM13352		Zea mays
33	371	42.1	182	3	AYF39857		Plant pol
34	371	42.1	206	1	ADX78919		Plant ful
35	371	42.1	206	2	ANO11441		Zea mays
36	371	42.1	225	1	ADY23237		Plant ful
37	371	42.1	225	2	ANO34177	Ano34177	
38	368	41.7	179	1	AAG38559		Arabidops
39	368	41.7	179	2	ALJ80333		Plant pro
40	368	41.7	179	2	ARN03104		Arabidops
41	368	41.7	225	2	ARN03103		Arabidops
42	364	41.3	182	2	ARM52453		Glycine m
43	359	40.7	177	1	ADT60317		Plant pol
44	359	40.7	177	2	AFC50108		Wheat ami
45	359	40.7	177	2	AJG83201	Ajg83201	Triticum

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 2 of 21

ALIGNMENTS

```
RESULT 1
AAY49960
    AAY49960 standard; protein; 177 AA.
XX
AC
    AAY49960:
XX
DT
    15-JUN-2007 (revised)
DT
    04-FEB-2000 (first entry)
XX
DE
    Human vesicle trafficking protein 3.
XX
KW Human; vesicle trafficking protein; VTP-1; VTP-2; VTP-3; apoptosis;
    cancer; inflammation; BOND_PC; coatomer protein complex, subunit zeta 1;
KW
KW
    CGI-120 protein; coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW COPZ1; COPZ; CGI-120; zeta1-COP; subunit zeta;
KW nonclathrin coat protein zetal-COP;
KW coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW 5930435A22Rik; AA407760; MGC118060;
KW
     similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW
    LOC609925; LOC607013;
KW
    coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW
    coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW
    unnamed protein product; unnamed protein product [Mus musculus];
KW
    hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW
    HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW
    Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW
    CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];
KW
    unnamed protein product [Macaca fascicularis];
KW
    Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW
     nonclathrin coat protein zeta-COP;
KW
     nonclathrin coat protein zeta-COP [Mus musculus]; Copzl protein;
```

http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010... 1/10/11

```
CC
     diseases such as cancer and inflammation, by administering a VTP
CC
     antagonist
CC
CC
     Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC
     information from BOND.
XX
SQ
     Sequence 177 AA;
  Ouerv Match
                          100.0%; Score 882; DB 1; Length 177;
  Best Local Similarity
                         100.0%;
  Matches 177; Conservative
                                0; Mismatches
                                                   0; Indels
                                                               0; Gaps
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
Qv
Db
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Qy
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Db
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
RESULT 2
AAB03815
ID
     AAB03815 standard; protein; 177 AA.
AC
     AAB03815;
XX
DT
     15-JUN-2007 (revised)
DT
     13-OCT-2000 (first entry)
XX
DE
     Human vesicle trafficking protein-3 (VTP-3) amino acid sequence.
XX
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010... 1/10/11
```

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Copz1 protein [Mus musculus]; G05783; G06886; G06888; G06890; G06891;

Novel vesicle trafficking proteins used in the diagnosis, prevention, and

designated VTP-3. VTPs can be used in a method for preventing or treating

The present sequence represents the human vesicle trafficking protein

disease associated with an increase in apoptosis. The method can treat

G016020; G030126; G030662; G05198; G08565.

97US-00967364.

97US-00967364.

PC:SWISSPROT; P61923, P61924, Q5R5F2.

treatment of inflammation or cancer.

Claim 9; Fig 7; 55pp; English.

Bandman O, Guegler KJ, Corley NC, Lal P, Shah P;

KW

KW

XX

PN

XX PD

XX PF

XX PR

XX

XX PI

XX DR

DR

DR

DR

DR

XX

PT PT

XX PS

CC

CC

CC

Homo sapiens.

US5989859-A.

23-NOV-1999.

07-NOV-1997:

07-NOV-1997;

(INCY-) INCYTE PHARM INC.

WPI: 2000-022782/02.

PC:NCBI; gi7706337.

N-PSDB; AAZ35835.

PC:BIND; 54453.

```
KW coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;
KW CGI-120; zetal-COP; subunit zeta; nonclathrin coat protein zetal-COP;
KW coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW 5930435A22Rik; AA407760; MGC118060;
KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW
    LOC609925; LOC607013;
KW
     coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW
     coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW
    unnamed protein product; unnamed protein product [Mus musculus];
KW
    hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW
    HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW
    Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW
     CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];
KW
    unnamed protein product [Macaca fascicularis];
KW
    Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW
    nonclathrin coat protein zeta-COP;
KW
     nonclathrin coat protein zeta-COP [Mus musculus]; Copzl protein;
KW
     Copz1 protein [Mus musculus]; G05783; G06886; G06888; G06890; G06891;
KW
     GO16020; GO30126; GO30662; GO5198; GO8565.
XX
OS
     Homo sapiens.
XX
PN
     US6071703-A.
XX
PD
     06-JUN-2000.
XX
PF
     04-AUG-1999;
                   99US-00368408.
XX
PR
     07-NOV-1997;
                   97US-00967364.
XX
PA
     (INCY-) INCYTE PHARM INC.
XX
PI
     Guegler KJ, Shah P, Corley NC, Bandman O, Lal P;
XX
DR
     WPI; 2000-422079/36.
DR
    N-PSDB; AAA59875.
DR
    PC:NCBI; gi7706337.
DR
     PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR
     PC:BIND: 54453.
XX
PT
     Identifying polynucleotides encoding vesicle trafficking proteins (VTP)
PT
     for treating and preventing e.g. inflammation, by detecting a
PT
     hybridization complex of a nucleic acid from a sample and a
PT
     polynucleotide encoding a VTP.
XX
PS
     Claim 1; Fig 7; 55pp; English.
XX
CC
     This sequence represents a human vesicle trafficking protein (VTP-3)
CC
     amino acid sequence. VTP-3 encoding cDNA was isolated from an aortic
CC
     tissue cDNA library (HEAONOTO3). VTP-3 has structural and chemical
CC
     homology with a subunit of cow coatomer protein, zeta COP. The present
CC
     invention relates to a method for detecting human VTP encoding
CC
     polynucleotide sequences and includes nucleotide and protein sequences
CC
    for human VTP-1, VTP-2 and VTP-3. Northern analysis of VTP-1, 2, and 3
CC
     shows that their expression is associated with cancer, inflammation and
CC
     foetal/infant development. The method of the invention is useful for
CC
     screening and identifying a polynucleotide encoding a human VTP, which
CC
     may be used for the diagnosis, prevention, or treatment of inflammation
CC
     associated disorder, e.g. asthma, Crohn's disease, diabetes, multiple
CC
     sclerosis, rheumatoid arthritis, infections, ulcerative colitis and
CC
     irritable bowel syndrome. Other diseases and disorders identified,
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010... 1/10/11
```

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Vesicle trafficking protein; VTP-3; human; cancer; inflammation; asthma;

foetal development; Crohn's disease; diabetes; multiple sclerosis;

irritable bowel syndrome; apoptosis; AIDS; Alzheimer's disease; KW Parkinson's disease; osteoporosis; wasting disorder; BOND_PC;

coatomer protein complex, subunit zeta 1; CGI-120 protein;

rheumatoid arthritis; infection; ulcerative colitis; proliferation;

KW

KW

KW

KW

```
CC
     those associated with cell proliferation or apoptosis, such as AIDS,
CC
     Alzheimer's disease, Parkinson's disease, osteoporosis, wasting diseases
CC
     and cancer
CC
CC
     Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC
     information from BOND.
XX
     Sequence 177 AA;
SO
  Query Match
                          100.0%; Score 882; DB 1; Length 177;
  Best Local Similarity 100.0%;
  Matches 177; Conservative
                               0; Mismatches
                                                  0; Indels
                                                               0: Gaps
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
Db
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Qv
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
          121 LFLAVDEIVDGGVILESDPOOVVHRVALRGEDVPLTEOTVSOVLOSAKEOIKWSLLR 177
Db
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
RESULT 3
AAB03789
ID
     AAB03789 standard; protein; 177 AA.
XX
AC
     AAB03789:
XX
DT
     15-JUN-2007 (revised)
DT
     26-OCT-2000 (first entry)
XX
DE
     Human capsid protein zeta-COP amino acid sequence.
XX
KW
    Human; capsid-protein; zeta-COP; BOND_PC;
KW
     coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW
     coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;
KW
     CGI-120; zetal-COP; subunit zeta; nonclathrin coat protein zetal-COP;
KW
    coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW
     5930435A22Rik; AA407760; MGC118060;
     similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW
KW
     LOC609925; LOC607013;
KW
     coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW
     coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW
    unnamed protein product; unnamed protein product [Mus musculus];
KW
    hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW
    HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW
     Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW
    CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];
KW
     unnamed protein product [Macaca fascicularis];
KW
     Coatomer protein complex, subunit zeta 1 [Mus musculus];
     nonclathrin coat protein zeta-COP;
KW
KW
     nonclathrin coat protein zeta-COP [Mus musculus]; Copzl protein;
KW
     Copzl protein [Mus musculus]; G05783; G06886; G06888; G06890; G06891;
KW
     GO16020; GO30126; GO30662; GO5198; GO8565.
XX
OS
     Homo sapiens.
XX
PN
     CN1248624-A.
XX
ΡD
     29-MAR-2000.
XX
PF
     22-SEP-1998;
                  98CN-00119744.
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010... 1/10/11
```

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prevented or treated with polynucleotide sequences encoding VTP include

```
PA
     (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
XX
PI
     Yu L, Tu O, Fu O;
XX
DR WPI; 2000-431993/38.
DR N-PSDB; AAA59847.
DR
    PC:NCBI; gi7706337.
DR
     PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR
     PC:BIND: 54453.
XX
PT
     Novel human capsid protein subunit coding sequence.
XX
PS
     Claim 2; Fig 2; 21pp; Chinese.
XX
CC
     This invention relates to a human gene encoding a capsid protein zeta
CC
     subunit (zeta-COP). The invention also relates to a zeta-COP protein
CC
     sequence. The present sequence represents the human zeta-COP protein
CC
     sequence
CC
CC
     Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC
     information from BOND.
XX
SQ Sequence 177 AA;
  Query Match
                          100.0%; Score 882; DB 1; Length 177;
  Best Local Similarity 100.0%;
  Matches 177; Conservative
                               0; Mismatches
                                                  0; Indels
                                                              0; Gaps
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
Db
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
Qу
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
          121 LFLAVDEIVDGGVILESDPOOVVHRVALRGEDVPLTEOTVSOVLOSAKEOIKWSLLR 177
QУ
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Dh
RESULT 4
AD023737
    ADO23737 standard; protein; 177 AA.
TD
XX
AC
     AD023737;
XX
DT 15-JUN-2007 (revised)
DT
    01-JUL-2004 (first entry)
XX
DE COPI coatomer protein, SEQ ID 26.
XX
    Cytostatic; nuclear envelope breakdown; nuclear pore protein; Nupl53;
KW
KW
    COPI coatomer complex; cancer; BOND_PC;
KW
     coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW
     coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;
KW
    CGI-120; zetal-COP; subunit zeta; nonclathrin coat protein zetal-COP;
KW
    coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW
    5930435A22Rik; AA407760; MGC118060;
KW
    similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW LOC609925; LOC607013;
KW coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW
     coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW
     unnamed protein product; unnamed protein product [Mus musculus];
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010... 1/10/11
```

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XX PR

XX

22-SEP-1998;

98CN-00119744.

```
DR
    PC:SWISSPROT; P61923, P61924, O5R5F2.
DR
     PC:BIND: 54453.
XX
PT
     New composition comprising a molecule that inhibits nuclear envelope
PT
     breakdown, useful in treating cancer, e.g. lymphoma, sarcoma or glioma.
XX
PS
     Claim 22; SEQ ID NO 26; 180pp; English.
XX
CC
     The present invention relates to a composition comprising a molecule that
CC
     inhibits nuclear envelope breakdown by interfering with the interaction
CC
     between nuclear pore protein Nupl53 and COPI coatomer complex. The
CC
     composition is useful in treating, inhibiting or preventing cancer, e.g.
CC
     lymphoma, leukaemia, mycosis fungoide, carcinoma, adenocarcinoma,
CC
    sarcoma, glioma, blastoma, neuroblastoma, plasmacytoma, histiocytoma,
CC
     melanoma, adenoma, hypoxic tumour, myeloma, AIDS-related lymphoma or AIDS
CC
     -related sarcoma or metastatic, bladder, brain or nervous system cancer,
CC
     glioblastoma or ovarian, skin or liver cancer, squamous cell carcinomas
CC
     of the mouth, throat, larynx, and lung or colon, cervical, breast,
CC
     epithelial, renal, genitourinary or pulmonary cancer, oesophageal
CC
     carcinoma, head and neck carcinoma or haematopoietic, testicular,
CC
     colorectal, prostatic or pancreatic cancer. The present sequence was used
CC
     to illustrate the invention.
CC
CC
     Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC
     information from BOND.
XX
so
    Sequence 177 AA;
                          100.0%; Score 882; DB 1; Length 177;
  Ouerv Match
  Best Local Similarity 100.0%;
  Matches 177; Conservative
                                0; Mismatches 0; Indels
                                                              0; Gaps
                                                                            0;
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
           1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
          61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
Qv
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010... 1/10/11
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hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;

HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens]; Coatomer protein complex, subunit zeta 1 [Homo sapiens];

unnamed protein product [Macaca fascicularis];

Ulmann KS, Liu J, Prunuske A, Dimaano C;

KW nonclathrin coat protein zeta-COP;

Copz1 protein [Mus musculus].

17-SEP-2003; 2003WO-US029267.

17-SEP-2002; 2002US-0411248P.

(UTAH) UNIV UTAH RES FOUND.

WPI; 2004-340314/31. N-PSDB; ADO23736.

PC:NCBI; gi4929709.

Unidentified.

01-APR-2004.

WO2004027381-A2.

CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];

Coatomer protein complex, subunit zeta 1 [Mus musculus];

nonclathrin coat protein zeta-COP [Mus musculus]; Copzl protein;

KW

KW

KW

KW

KW

KW

KW

XX OS

XX PN

XX PD

XX

PF XX PR

XX

PA XX PI

XX DR

DR DR

```
KW
     unnamed protein product; unnamed protein product [Mus musculus];
KW
    hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW
     HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW
     Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW
    CGI-120 protein [Homo sapiens]; zetal-COP [Homo sapiens];
KW
     unnamed protein product [Macaca fascicularis];
KW
     Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW
     nonclathrin coat protein zeta-COP;
KW
     nonclathrin coat protein zeta-COP [Mus musculus]; Copzl protein;
     Copz1 protein [Mus musculus]; G05783; G06886; G06888; G06890; G06891;
KW
KW
     G016020; G030126; G030662; G05198; G08565.
XX
OS
     Homo sapiens.
XX
PN
     CN1618808-A.
XX
PD
     25-MAY-2005.
XX
PF
     21-NOV-2003; 2003CN-10108764.
XX
PR
     21-NOV-2003; 2003CN-10108764.
XX
PA
     (SHAN-) SHANGHAI HUMAN GENOME RES CENT.
XX
PΙ
     Zhu Z, Han Z;
XX
DR
     WPI; 2005-640540/66.
DR
     SWISSPROT; Q9Y3C3.
DR
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DR
     PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR
     PC:BIND; 54453.
XX
PT
     Liver cancer related protein and its coding sequence and use.
XX
PS
     Claim 1; SEO ID NO 63; 26pp; Chinese.
XX
CC
     The invention describes a novel liver cancer associated protein, the
CC
     polynucleotide for coding it, the process for preparing said protein by
CC
     recombination, and the application of said polynucleotide. This is the
CC
     amino acid sequence of a liver cancer associated protein.
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 8 of 21

121 LFLAVDEIVDGGVILESDPOOVVHRVALRGEDVPLTEOTVSOVLOSAKEOIKWSLLR 177

121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

protein production; recombinant DNA; liver tumor; cvtostatic; neoplasm;

coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;

CGI-120; zetal-COP; subunit zeta; nonclathrin coat protein zetal-COP;

coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;

similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);

coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];

coatomer protein complex, subunit zeta 1; CGI-120 protein;

coatomer protein complex, subunit zeta 1, isoform CRA_a;

Οv

Db

XX AC

XX

DT

XX DE

XX

KW

RESULT 5 AEJ65021 ID AEJ

AEJ65021;

15-JUN-2007 (revised)

LOC609925; LOC607013;

05-OCT-2006 (first entry)

AEJ65021 standard; protein; 177 AA.

gastrointestinal disease; BOND_PC;

5930435A22Rik; AA407760; MGC118060;

Liver cancer associated protein SEQ ID NO 63.

```
CC
     Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC
    information from BOND.
XX
SO
     Sequence 177 AA;
  Ouerv Match
                         100.0%; Score 882; DB 2; Length 177;
  Best Local Similarity 100.0%;
  Matches 177; Conservative
                                0; Mismatches
                                                  0; Indels
                                                              0; Gaps
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Db
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
         121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Qv
Db
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RESULT 6
AYT11804
ID AYI11804 standard; protein; 177 AA.
XX
AC
    AYI11804;
XX
DT
    28-OCT-2010 (first entry)
XX
DE
    Human coatomer subunit zeta-1 protein, SEQ ID 29.
XX
KW
    Bio-nanoparticle element; Coatomer subunit zeta-1; nanotechnology;
KW
    BOND_PC; coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW
    COPZ1; COPZ; CGI-120; zetal-COP; subunit zeta;
     nonclathrin coat protein zetal-COP; D4Ertd360e; 5930435A22Rik; AA407760;
KW
KW
    MGC118060;
KW similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW LOC609925; LOC607013; similar to CGI-120 protein;
KW
    PREDICTED: similar to CGI-120 protein [Equus caballus]; LOC100064590;
KW
    Copz1_predicted;
    similar to Coatomer subunit zeta-1 (Zeta-1-coat protein) (Zeta-1 COP);
KW
KW
     LOC100156765; Coatomer subunit zeta-1; DKFZp469A0331;
    coatomer protein complex, subunit zeta 1, isoform CRA a;
KW
KW
     unnamed protein product; hypothetical protein; HSPC181; z-cop;
KW
     nonclathrin coat protein zeta-COP; Copzl protein; GO5783; GO6886; GO6888;
KW
    G06890; G06891; G016020; G030126; G030662; G05198; G08565.
YY
OS
    Homo sapiens.
XX
PN
    US2010226856-A1.
XX
PD
     09-SEP-2010.
XX
PF
     06-MAR-2009; 2009US-00399906.
XX
PR
     06-MAR-2009; 2009US-00399906.
XX
PA
    (VITA/) VITALIANO F.
PA
    (VITA/) VITALIANO G.
XX
PΙ
    Vitaliano F, Vitaliano G;
XX
DR
    WPI; 2010-L54477/62.
     SWISSPROT; P61923.
DR
DR
    PC:NCBI; qi7706337.
```

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 9 of 21

```
CC
     recombinant amino acid molecule elements and their residue elements. The
CC
     invention also provides a method for forming a dynamic bio-nanoparticle
CC
     element. The dynamic bio-nanoparticle element is useful in a
CC
     multifunction nanoscale bio-nanoparticle platform such as a biomedical
CC
     platform, bio-molecular platform, electronics platform and information
CC
     processing platform. The dynamic bio-nanoparticle element provides self-
CC
     directing, self-replicating, self-adapting, self-repairing, self-
CC
     regulating and self-regenerating methods for one or more minimalist, non-
CC
     cage elements, which can also perform on-the-fly target prioritization.
CC
     The present sequence is a human coatomer subunit zeta-1 protein used in
CC
     the method for forming a dynamic bio-nanoparticle element of the
CC
     invention.
CC
CC
     Revised record issued on 13-OCT-2010 : Enhanced with precomputed
CC
     information from BOND.
XX
SO
     Sequence 177 AA;
                          100.0%; Score 882; DB 3; Length 177;
  Query Match
  Best Local Similarity 100.0%;
  Matches 177; Conservative
                                                 0; Indels
                                0; Mismatches
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Qу
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Dh
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Qv
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Db
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
RESULT 7
AD057263
ID
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XX
AC
     AD057263;
XX
DT
     15-JUN-2007 (revised)
DT
     15-JUL-2004 (first entry)
XX
DE
     Kidney development associated protein seqid 30.
XX
KW
     nephrotropic; cardiant; antiinfertility; cerebroprotective;
KW
     neuroprotective; muscular; cytostatic; osteopathic; gene therapy;
KW
     kidney development; kidney disorder; developmental disorder;
KW
     circulatory disorder; hearing disorder; heart defect; infertility;
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010...
```

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 10 of 21

New dynamic bio-nanoparticle element, useful in a multifunction nanoscale

bio-nanoparticle platform, such as a biomedical platform, bio-molecular

useful in a multifunction nanoscale bio-nanoparticle platform. The bio-

coatomer cage element, having attributes, properties, characteristics,

compositions, behaviors and capabilities, that differ in respect from a

fully assembled clathrin or coatomer cage element and nanoscale elements

platform, electronics platform, and information processing platform.

The present invention relates to a dynamic bio-nanoparticle element

nanoparticle element comprises a clathrin or coatomer cage subset

element, forming in vitro less than a fully assembled clathrin or

of types formed in whole or in part from purified, synthetic or

DR

DR

XX PT

PT

PT

XX PS

CC

CC

CC

CC

CC

CC

CC

CC

PC:SWISSPROT; P61923, P61924, O5R5F2.

Claim 1; SEQ ID NO 29; 121pp; English.

PC:BIND: 54453.

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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 11 of 21
KW
     stroke; mental retardation; muscle defect; proliferative disorder;
KW
     bone defect; bone disorder; zebrafish; BOND_PC; zetal-cop;
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zetal-cop [Danio rerio]; copz1; CHUNP6876;
KW
    nonclathrin coat protein zetal-COP;
KW
    nonclathrin coat protein zetal-COP [Danio rerio]; GO6810; GO6886;
KW
    G030662; G08565; G019012.
XX
OS
     Danio rerio.
XX
PN
     US2004068763-A1.
XX
PD
     08-APR-2004.
XX
PF
     28-MAR-2003; 2003US-00403571.
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PR 29-MAR-2002; 2002US-0368760P. XX PA (HOPK/) HOPKINS N. PA (GOLL/) GOLLING G.

KW

XX

PT

XX PS

XX CC

CC

CC

CC

CC

Qv

(AMST/) AMSTERDAM A. PA PA (SUNZ/) SUN Z. XX PI Hopkins N. Golling G. Amsterdam A. Sun Z; XX

DR WPI; 2004-304692/28. DR N-PSDB; AD057262. DR PC:NCBI; gi18858455. XX PT New 459 nucleic acids and encoded polypeptides, useful for diagnosing, PT

development associated protein.

treating or preventing a kidney disorder in an organism, or in screening for compounds that modulate the development of an organism. Disclosure; SEQ ID NO 30; 347pp; English. The invention describes an isolated nucleic acid molecule (I) comprising

sequence of 2808 base pairs (SEQ ID NO: 59) given in the specification, CC over at least 600 contiguous base pairs, where the nucleic acid functions CC in kidney development. (I) is useful for treating or preventing a kidney CC disorder in an organism, where the nucleic acid elicits an alteration in CC expression of a 459 nucleic acid sequence in the organism and CC subsequently treats or prevents a kidney disorder. The nucleic acid may CC also be used in diagnosing, preventing and treating a variety of CC mammalian diseases and developmental disorders (e.g. circulatory CC disorders, hearing disorders, heart defect, infertility, stroke, mental CC retardation, muscle defects, proliferative disorders, or bone defects or CC disorders) as well as in screening for compounds that modulate the CC development of an organism as a whole or of specific tissues or organs CC within that organism. This is the amino acid sequence of a kidney

a sequence having at least 75% sequence identity to the 459 nucleic acid

CC Revised record issued on 15-JUN-2007 : Enhanced with precomputed CC information from BOND. XX SQ Sequence 177 AA;

Query Match

Best Local Similarity 93.2%; Matches 165; Conservative 11; Mismatches 1; Indels 0; Gaps

1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60 1 MDTLILEPSLYTVKAVLIMDNDGERLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60

95.8%; Score 845; DB 1; Length 177;

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Db 61 LLEGLTVVYKSNIDLYFYVIGSSHENELMLMSVLNCLFDSLSOMLRKNVEKRALLENMEG 120

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RESULT 8
AAY31641
     AAY31641 standard; protein; 210 AA.
TD
YY
AC
     AAY31641;
XX
DT
     02-NOV-1999 (first entry)
XX
DE
     Human transport-associated protein-3 (TRANP-3).
XX
KW
     Transport-associated protein; TRANP; nuclear pore; nuclear transport;
KW
     vesicle trafficking; cancer; cystic fibrosis; multidrug resistance;
KW
     hypercholesterolaemia; diagnosis; treatment.
XX
OS
     Homo sapiens.
XX
FH
     Kev
                      Location/Oualifiers
FT
     Modified-site
FT
                      /note= "0-phosphorylated by tyrosine kinase"
FT
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FΤ
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                      /note= "O-phosphorylated by casein kinase II or protein
FT
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FT
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                      83
FT
                      /note= "N-glvcosvlated"
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                      /note= "O-phosphorylated by casein kinase II"
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FT
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FT
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FT
                      /note= "O-phosphorylated by casein kinase II or protein
FT
                      kinase C"
XX
PN
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XX
PD
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XX
PF
     05-FEB-1999;
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XX
PR
                    98US-00021764.
     11-FEB-1998;
XX
PA
     (INCY-) INCYTE PHARM INC.
XX
PΙ
     Au-Young J, Hillman JL, Lal P, Guegler KJ, Corley NC, Yue H;
PI
     Bandman O, Baughn MR;
XX
DR
     WPI: 1999-508646/42.
DR
     N-PSDB; AAZ11733.
XX
PT
     Human TRANP coding sequences, used to treat transport disorders and
PT
     cancer.
XX
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2277&ItemName=2010...
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 12 of 21

121 LFLAVDEIVDGGVILESDPOOVVHRVALRGEDVPLTEOTVSOVLOSAKEOIKWSLLR 177

121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177

Qy Dh Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103255_us-09-556-178-5 rpr

Description

coatomer zeta chai

```
GenCore version 6.3
Copyright (c) 1993 - 2010 Biocceleration Ltd.
```

OM protein - protein search, using sw model

December 14, 2010, 11:24:11 ; Search time 2 Seconds

(without alignments) 7139.284 Million cell updates/sec

US-09-556-178-5 882

1 MEALILEPSLYTVKAILILD.......gTVSQVLQSAKEQIKWSLLR 177 Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Post-processing: Minimum Match 04

Listing first 45 summaries

Database : PIR 80:*

Query Score Match Length DB ID No. 99.2

875

2	499		184	2	T23002	hypothetical prof
3	344	39.0	162		C96635	probable coatome:
4	308	34.9	189	2	352521	coatomer protein
5	299.5	34.0		2		coatomer zeta sul
6	267	30.3	153	2	T01831	hypothetical prof
7	141.5	16.0	145	2	T08407	clathrin coat as:
8	118	13.4	143	2	B84581	probable clathri
9	117	13.3	446	2	359646	clathrin coat as:
1.0	116	13.2	194	2		YAP19 protein hor
11	112.5	12.8	141		C71605	clathrin coat as
1.2	108	12.2	157	2	T31801	hypothetical prof
1.3	106.5	12.1	143	2	T40635	clathrin coat as:
1.4	99	11.2	165	2	862563	adaptin complex
15	98	11.1	1472	2	367195	probable membrane
16	97.5	11.1	441		B49837	clathrin-associat
17	90.5	10.3	214	2	\$51405	synaptobrevin SE
1.8	90	10.2	1271	2	T08607	hypothetical pro-
1.9	88.5	10.0	290	2	C96911	transcription re-
20	87.5	9.9	475	2	365290	clathrin-associat
21	86	9.8	158	2	A40535	clathrin-associat
22	86	9.8	161	2	E84551	clathrin assembly
23	86	9.8	162	2	T06116	probable clathri
24	85.5	9.7	663	2	B70460	excinuclease ABC
25	85.5	9.7	699	2	T18984	hypothetical pro-
26	85	9.6	380	2	D64129	probable 8-amino
27	84.5	9.6	439	2	378378	maturase-like pro
28	84.5	9.6	863	2	B72344	tRNA nucleotidyl
29	84	9.5	132	2	T02991	clathrin coat as:
3.0	84	9.5	142	2	T15957	hypothetical pro-
3.1	83.5	9.5	412	2	E97736	mitochondrial pro
3.2	83	9.4	142	2	B40535	clathrin-associat
3.3	83	9.4	156	2	837757	clathrin-associat
3.4	83	9.4	410	2	364451	hypothetical pro-
3.5	83	9.4	896	2	T47645	centromere prote:
36	82.5	9.4	324	2	C90492	hypothetical prof
37	82.5	9.4	569	1	D64215	conserved hypothe
3.8	82.5	9.4	909	2	AG3314	excinuclease ABC
39	82.5	9.4	1104	2	836773	GTPase-activating
40	82	9.3	416	2	D70347	cell division pro
41	82	9.3	659		G81334	probable N-acety
42	82	9.3	686	2	T23721	hypothetical pro-
4.3	82	9.3	725	2	G90555	vacb-like (shige
44	82	9.3	803	1	E70041	probable copper-

SUMMARIES

\$1.TONMENTS

```
RESULT 1
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A49465

C:Species: Bos prinigenius taurus (cattle) C:Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004 C:Accession: A49465

CiAccession: A69450
RR(Nos, O.; Hara-Rupe, S.; Orci, L.; Ravazzola, M.; Amharcit, M.; Tamigawa, G.; Kieland, F.T.; Rothman, J.E.
J. Cell Baol. 123, 1727-1734, 1993
A; Title: rate-Cry, a subunit of coatomer, is required for COP-coated wesicle assembly.
A; Reference number: A49465; MOID: 94103128; PMID: 8276893
A; Accession: A89404

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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103255_us-09-5... Page 2 of 7
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A)(Tross-references: UNIPROT:P35604; UNIPARC:UPI0000127EF0; GB:X75935; NID:g441485; PIDN:CAA53539.1; PID:g441486

C; Superfamily: Vesicle coat complex COPI, seta subunit

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Best Local Similarity 98.9%;
                                                          1; Mismatches 1; Indels 0; Gaps 0;
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                   61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
                   61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMTVLNCLFDSLSOMLRKNVEKRALLENMEG 120
                  121\ \mathsf{LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKDQIKWSLLR}\ 177
                  121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
hynothetical protein F59E18.3 - Caenorhabditis elegans
ogrocies: Caenorhabditis elegans
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
submitted to the EMBL Data Library, September 1994
A:Reference number: 219650
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A - Residues : 1-184 - NTL
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A;Experimental source: clone F59E10
AlGene: CESP:F59E10.3
A/Map position: 2
A/Map tosition: 2
A/Introns: 6/3; 30/3; 60/1; 135/2
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   Query Natch 56.6%; Score 499; DB 2; Length 184;
Best Local Similarity 54.9%;
Natches 96; Conservative 49; Mismatches 29; Indels 6; Gaps 3;
                    9 SLYTVKAILILONDGDRLFAKYYD-DTYPSVKEQKAFEKNIFNKTHR-TDSEIALLEGLT 66
                   67 VVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEGLFLAVD 126
                   70 CLYRSNVDLYFYVLGSTRENELFLDATLTCLYDAVSVVLRKNVEKKALIDSMDTIMLIID 129
                  127 EIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQV----LQSAKEQIKWSLLR 175
                  130 EICDEGIIMETDAQAVVQRTALKSDEVSFSDQSVSQIGFSFMKSANEQFKWSLLK 184
RESULT 3
probable coatomer zeta subunit T7P1.11 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96635
RyTheologia, A.; Exker, J.R.; Falm, C.I.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, I
Nature 408, 816-820, 2000
Abdubness Hester, J.L.; Senkins, J.; Johnson-Hogson, C.; Mann, S.; Haykin, E.; Kim, C.J.; Koo, H.L.; Kreenestekaia, I.; Kutt, D.B.; Dann, A.; Lam, B.; Langin-Ho-Abdubness Salberg, J.L.; Senkins, J., Salburness Salberg, J.J.; Senkins, J., Salburness Salberg, J.J.; Senkins, J., Salburness Salberg, J., Salburness Salburness, J., Salbur
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A:Residues: 1-162 <STO
A;Cross-references: UNIPROT:Q9C956; UNIPARC:UPI000009CDAC; GB:AE005173; NID:g6751687; PIDN:AAF27670.1; GSPDB:GN00141
C; Superfamily: Vesicle coat complex COPI, seta subunit
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Best Local Similarity 45.4%;
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                     7 VKNILLLOSEGKRVAVKYYSDDWPTNSAQEAFEKSVFTKTQKTNARTEVEVTALENNIVV 66
                   69 YKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEGLFLAVDEI 128
                   67 YKFYDDLHFFYTGGEENELILASVLEGLFDAYTLLLRSNYDKREALDNLDLIFLSFOEI 126
                  129 VDGGVILESDPQQVVHRVALRGED--VPL7BQ 158
                  127 IDGGIVLETDANVIAGKAGINSTOPNAPLSEQ 158
coatomer protein zeta chain - yeast (Saccharomyces cerevisiae)
Njälternate names: protein LPA7w; protein YPB132.03; protein YPL010w; zeta-COP
C/Species: Saccharomyces cerevisiae
```

A;Cross-references: UNIPROT:P53600; UNIPARC:UPI000005319F; EMBL:E48483; NIO:g683777; PION:CAA88376.1; PID:g683780; MIPS:YPL010w

C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004 C;Accession: 352521; 359681; JC5152

R; Badcock, K.; Churcher, C.

A: Molecule type: DNA A: Residues: 1-189 < RADA

submitted to the EMBL Data Library, February 1995

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 1 of 25

SCORE Search Results Details for Application 09556178 and Search Result 20101214 103254 us-09-556-178-5.rup.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214 103254 us-09-556-178-5.rup.

Go Back to previous page

GenCore version 6.3 Copyright (c) 1993 - 2010 Biocceleration Ltd.

OM protein - protein search, using sw model

December 14, 2010, 11:23:42; Search time 96 Seconds Run on:

(without alignments) 7637.199 Million cell updates/sec

US-09-556-178-5

Title: Perfect score: 882

1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177 Sequence:

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

12869322 segs, 4158259533 residues

Total number of hits satisfying chosen parameters: 12869322

Minimum DB seg length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Database : UniProt 201011:*

1: uniprot_sprot:* 2: uniprot_trembl:*

CIMMADDIEC

				SUMMARIES	
	%				
	Query				
Score	Match	Length	DB	ID	Description
	100.0				DC1003 D W
					P61923 RecName: Fu
					P61924 RecName: Fu
882	100.0	177	1	COPZ1_PONAB	Q5r5f2 RecName: Fu
882	100.0	177	2	D4A8T3_RAT	D4a8t3 SubName: Fu
882	100.0	177	2	Q542M2_MOUSE	Q542m2 SubName: Fu
878	99.5	177	1	COPZ1_BOVIN	P35604 RecName: Fu
877	99.4	177	2	Q53FU3_HUMAN	Q53fu3 SubName: Fu
847	96.0	177	2	Q28HL1_XENTR	Q28hll SubName: Fu
846	95.9	177	2	AOAUT9_XENLA	A0aut9 SubName: Fu
846	95.9	187	2	Q801P3_XENLA	Q801p3 SubName: Fu
845	95.8	177	2	Q9IB48_DANRE	Q9ib48 SubName: Fu
843	95.6	177	2	Q6GQG0_XENLA	Q6gqg0 SubName: Fu
842	95.5	177	2	Q7SXH1_DANRE	Q7sxh1 SubName: Fu
836	94.8	177	2	C3KJY4_ANOFI	C3kjy4 SubName: Fu
832	94.3	177	2	B5X5K5_SALSA	B5x5k5 SubName: Fu
	882 882 882 882 882 877 847 846 846 845 843 842 836	Score Match 882 100.0 882 100.0 882 100.0 882 100.0 882 100.0 882 100.0 882 100.0 883 100.0 884 99.5 877 99.4 847 96.0 846 95.9 846 95.9 846 95.9 848 95.6 842 95.5 843 95.6 842 95.5	Ouery Score Match Length 882 100.0 177 882 100.0 177 882 100.0 177 882 100.0 177 882 100.0 177 882 100.0 177 884 99.5 177 847 96.0 177 846 95.9 177 846 95.9 177 846 95.9 177 845 95.8 177 843 95.6 177 842 95.5 177 843 95.6 177	Score Match Length DB 882 100.0 177 1 882 100.0 177 1 882 100.0 177 1 882 100.0 177 2 882 100.0 177 2 882 100.0 177 2 882 100.0 177 2 882 100.0 177 2 8847 99.5 177 1 847 96.0 177 2 846 95.9 177 2 846 95.9 177 2 846 95.9 177 2 848 95.6 177 2 843 95.6 177 2 842 95.5 177 2 843 95.6 177 2	Query Score Match Length DB ID

_					· r · ·				
	16	832	94.3	179	2	C1BY80_ESOLU	C1by80	SubName:	Fu
	17	828	93.9	177	2	B5X8E4 SALSA	B5x8e4	SubName:	Fu
	18	828	93.9	177	2	C1BHI5_ONCMY	C1bhi5	SubName:	Fu
	19	828	93.9	177	2	C3KJ46_ANOFI	C3kj46	SubName:	Fu
	20	825	93.5	177	2	B9EM01_SALSA	B9em01	SubName:	Fu
	21	819	92.9	175	2	C1BFE7 ONCMY	C1bfe7	SubName:	Fu
	22	815	92.4	174	2	B5X954 SALSA	B5x954	SubName:	Fu
	23	814	92.3	177	2	C1BH82_ONCMY	Clbh82	SubName:	Fu
	24	813	92.2	163	2	Q8R3M1_MOUSE	Q8r3m1	SubName:	Fu
	25	810	91.8	177	2	B5XDE2_SALSA	B5xde2	SubName:	Fu
	26	745.5	84.5	154	2	B4DDX8_HUMAN	B4ddx8	SubName:	Fu
	27	701.5	79.5	173	2	Q9IB47_DANRE	Q9ib47	SubName:	Fu
	28	692	78.5	189	2	Q6DKF5_DANRE	Q6dkf5	SubName:	Fu
	29	683.5	77.5	229	2	C3XTB6_BRAFL	C3xtb6	SubName:	Fu
	30	673.5	76.4	178	2	B9EQ95_SALSA	B9eq95	SubName:	Fu
	31	673	76.3	179	2	B9EPB0_SALSA		SubName:	
	32	673	76.3	210	1	COPZ2_HUMAN		RecName:	
	33	667	75.6	205	1	COPZ2_MOUSE	Q9jhh9	RecName:	Fu
	34	666.5	75.6	178	2	C1BHL1_ONCMY	C1bhl1	SubName:	Fu
	35	664	75.3	203	2	C1BFJ5_ONCMY		SubName:	
	36	663	75.2	185	2	Q9CTG7_MOUSE		SubName:	
	37	649	73.6	156	2	Q6P383_XENTR		SubName:	
	38	625.5	70.9	178	2	EOVA85_PEDHC		SubName:	
	39	623	70.6	183	2	A7S1DO_NEMVE	A7s1d0	SubName:	Fu
	40	621.5	70.5	177	2	Q16K41_AEDAE		SubName:	
	41	620.5	70.4	177	2	BOW863_CULQU		SubName:	
	42	620.5	70.4	182	2	D6WPS8_TRICA		SubName:	
	43	620	70.3	181	2			SubName:	
	44	619.5	70.2	178	2	C4WUX3_ACYPI	C4wux3	SubName:	Fu

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 2 of 25

ALIGNMENTS

Q7q5c2 SubName: Fu

```
RESULT 1
COPZ1 HUMAN
ID COPZ1_HUMAN
                            Reviewed;
                                              177 AA.
AC
    P61923; Q549N6; Q9Y3C3;
DT 07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT 07-JUN-2004, sequence version 1.
DT 05-OCT-2010, entry version 66.
DE
   RecName: Full=Coatomer subunit zeta-1;
DE
    AltName: Full=Zeta-1-coat protein;
DE
             Short=Zeta-1 COP;
GN
   Name=COPZ1; Synonyms=COPZ; ORFNames=CGI-120, HSPC181;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC 
    Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC
    Catarrhini; Hominidae; Homo.
OX
    NCBI TaxID=9606;
RN
    [1]
RP
    NUCLEOTIDE SEQUENCE [MRNA].
RX
    MEDLINE=20512057; PubMed=11056392;
RA
     Futatsumori M., Kasai K., Takatsu H., Shin H.-W., Nakayama K.;
RT
     "Identification and characterization of novel isoforms of COP I
RT
     subunits.";
RL
    J. Biochem. 128:793-801(2000).
RN
    [2]
RP
    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX
    MEDLINE=20272150; PubMed=10810093; DOI=10.1101/gr.10.5.703;
RA
     Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
RT
     "Identification of novel human genes evolutionarily conserved in
RT
    Caenorhabditis elegans by comparative proteomics.";
RL
    Genome Res. 10:703-713(2000).
```

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

69.4 177 2 Q7Q5C2_ANOGA

45 612.5

RN RP

http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11

```
RX PubMed=15489334; DOI=10.1101/gr.2596504;
RG
    The MGC Project Team;
RT
     "The status, quality, and expansion of the NIH full-length cDNA
RT
     project: the Mammalian Gene Collection (MGC).";
RL
     Genome Res. 14:2121-2127(2004).
RN
RP
     PROTEIN SEQUENCE OF 1-14, ACETYLATION AT MET-1, AND MASS SPECTROMETRY.
    TISSUE=Colon carcinoma;
RC
RA
    Bienvenut W.V., Zebisch A., Kolch W.;
RL Submitted (DEC-2008) to UniProtKB.
RN
    181
RP
    PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-161, AND MASS
RP
    SPECTROMETRY.
RC
    TISSUE=Embryonic kidney;
RX
    PubMed=17525332; DOI=10.1126/science.1140321;
RA
     Matsuoka S., Ballif B.A., Smogorzewska A., McDonald E.R. III,
RA
    Hurov K.E., Luo J., Bakalarski C.E., Zhao Z., Solimini N.,
RA
     Lerenthal Y., Shiloh Y., Gygi S.P., Elledge S.J.;
RT
     "ATM and ATR substrate analysis reveals extensive protein networks
RT
    responsive to DNA damage.";
RL
     Science 316:1160-1166(2007).
RN
RP
     IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RA
     Colinge J., Superti-Furga G., Bennett K.L.;
     Submitted (OCT-2008) to UniProtKB.
RL
RN
RP
     ACETYLATION [LARGE SCALE ANALYSIS] AT MET-1, AND MASS SPECTROMETRY.
RC
     TISSUE=Embryonic kidney;
RX
     PubMed=19413330; DOI=10.1021/ac9004309;
    Gauci S., Helbig A.O., Slijper M., Krijgsveld J., Heck A.J.,
RA
RA
    Mohammed S.;
RT
     "Lys-N and trypsin cover complementary parts of the phosphoproteome in
    a refined SCX-based approach.";
RT
RL
    Anal. Chem. 81:4493-4501(2009).
RN
RP
     STRUCTURE BY NMR.
RA
     Yu W., Jin C., Xia B.;
RT
     "The NMR structure of human zeta-COP.";
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
```

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 3 of 25

TISSUE=Umbilical cord blood;

stem/progenitor cells.";

NUCLEOTIDE SEQUENCE [MRNA].

Genome Res. 10:1546-1560(2000).

RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200; Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,

Tu Q., Yu L., Hu P.R., Zhang H.L., Huang J., Zhao S.Y.;

Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L.,

Hannenhalli S., Turner R., Yooseph S., Lu F., Nusskern D.R., Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,

Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,

"Cloning and functional analysis of cDNAs with open reading frames for

"Cloning and expression of a new human cDNA homology to B.taurus z-cop

Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R., Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,

Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,

Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,

Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;

300 previously undefined genes expressed in CD34+ hematopoietic

RX

RA

RA RA

RT

RT

RT

RI.

RN [4] RP NUC

RA

RT

RT mRNA.";

RL

RN RP

RA

RA

RA RA

RA RA

RA

RA

RL Sub RN [6]

Venter J.C.;

RC TISSUE=Placenta;

```
SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 4 of 25
```

-!- FUNCTION: The coatomer is a cytosolic protein complex that binds to dilysine motifs and reversibly associates with Golgi non-

clathrin-coated vesicles, which further mediate biosynthetic

network. Coatomer complex is required for budding from Golgi

transport of dilysine-tagged proteins. In mammals, the coatomer

also influences the Golgi structural integrity, as well as the

can only be recruited by membranes associated to ADP-ribosylation

factors (ARFs), which are small GTP-binding proteins; the complex

membranes, and is essential for the retrograde Golgi-to-ER

protein transport from the ER, via the Golqi up to the trans Golqi

RL

CC

CC

CC

CC

CC

CC

CC

CC

CC

Submitted (JUN-2007) to the PDB data bank.

```
CC
       processing, activity, and endocytic recycling of LDL receptors (By
CC
        similarity).
CC
     -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC
        assembly and, hence, the rate of biosynthetic protein transport
CC
         due to its association-dissociation properties with the coatomer
CC
CC
     -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC
        beta, beta', gamma, delta, epsilon and zeta subunits.
CC
     -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus
CC
        membrane; Peripheral membrane protein; Cytoplasmic side (By
CC
         similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC
         Peripheral membrane protein; Cytoplasmic side (By similarity).
        Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
CC
CC
        side of the Golgi, as well as on the vesicles/buds originating
CC
        from it (By similarity).
CC
     -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR.
CC
     -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC
CC
     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC
     Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AB047848; BAB17659.1; -; mRNA.
DR
    EMBL; AF151878; AAD34115.1; -; mRNA.
    EMBL; AF161529; AAF29144.1; -; mRNA.
DR
DR EMBL; AF086911; AAP97141.1; -; mRNA.
DR EMBL; CH471054; EAW96774.1; -; Genomic_DNA.
DR EMBL; BC002849; AAH02849.1; -; mRNA.
DR IPI; IPI00032851; -.
DR RefSeg; NP 057141.1; -.
DR UniGene; Hs.505652; -.
DR PDB; 2HF6; NMR; -; A=1-149.
DR PDBsum; 2HF6; -.
DR
   ProteinModelPortal; P61923; -.
DR
    DIP; DIP-29873N; -.
DR
    IntAct; P61923; 3.
DR STRING; P61923; -.
DR PhosphoSite; P61923; -.
DR PRIDE; P61923; -.
DR Ensembl; ENST00000262061; ENSP00000262061; ENSG00000111481.
DR GeneID; 22818; -.
DR KEGG; hsa:22818; -.
DR UCSC; uc001sfs.1; human.
DR CTD; 22818; -.
DR
    GeneCards; GC12P054718; -.
DR
    H-InvDB; HIX0010694; -.
DR
    HGNC; HGNC: 2243; COPZ1.
DR PharmGKB; PA26760; -.
DR eggNOG; prNOG08087; -.
DR HOGENOM; HBG326766; -.
DR HOVERGEN; HBG051077; -.
DR InParanoid; P61923; -.
DR OMA; YDDTYPT; -.
DR PhylomeDB; P61923; -.
DR Reactome; REACT 11123; Membrane Trafficking.
DR
    NextBio; 43208; -.
DR
     ArrayExpress; P61923; -.
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```

```
FT
    HELIX
                  88
                        105
FT
     HELIX
                 111
                        115
FT
     HELIX
                 118
                        128
FT HELIX
                 139
                        148
                          100.0%; Score 882; DB 1; Length 177;
  Query Match
  Best Local Similarity 100.0%;
  Matches 177; Conservative
                                0; Mismatches
                                                   0: Indels
                                                                 0; Gaps
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
Db
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
Qу
Dh
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Db
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
COPZ1 MOUSE
ID
    COPZ1_MOUSE
                             Reviewed:
                                               177 AA.
AC
     P61924; Q9Y3C3;
     07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT
DT
     07-JUN-2004, sequence version 1.
DT
     05-OCT-2010, entry version 58.
DE
    RecName: Full=Coatomer subunit zeta-1;
DE
     AltName: Full=Zeta-1-coat protein;
DE.
              Short=Zeta-1 COP;
GN
     Name=Copz1; Synonyms=Copz;
0S
     Mus musculus (Mouse).
0C
     Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010...
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 5 of 25

DR

DR

DR

DR

DR

DR

ΠR

DR

PE

KW

KW

KW

KW

FT CHAIN

FT

FT

FT

FT STRAND

FT STRAND

FT HELIX

FT STRAND

FT STRAND

FT STRAND

Transport.

MOD_RES

MOD_RES

Baee; P61923; -.

CleanEx; HS_COPZ1; -.

Genevestigator; P61923; -.

GermOnline; ENSG00000111481; Homo sapiens.

GO; GO:0005829; C:cvtosol; EXP:Reactome.

InterPro; IPR022775; AP_mu_sigma_su.

InterPro; IPR011012; Longin-like.

Pfam; PF01217; Clat_adaptor_s; 1.

SUPFAM; SSF64356; Longin_like; 1.

1: Evidence at protein level;

161 161

14

25 30

38 52

59 62

65

75 81

PROSITE; PS00989; CLAT ADAPTOR S; 1.

InterPro; IPR000804; Clathrin_sm-chain_CS.

177

1

20

GO; GO:0030126; C:COPI vesicle coat; IDA:UniProtKB.

GO; GO:0048205; P:COPI coating of Golgi vesicle; EXP:Reactome.

3D-structure; Acetylation; Complete proteome; Cytoplasm;

Golgi apparatus; Membrane; Phosphoprotein; Protein transport;

GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.

Cytoplasmic vesicle; Direct protein sequencing; ER-Golgi transport;

GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; IDA:UniProtKB.

GO; GO:0006890; P:retrograde vesicle-mediated transport, Golq. . .; TAS:UniProtKB.

Coatomer subunit zeta-1.

/FTId=PRO 0000193825.

N-acetylmethionine.

Phosphoserine.

GO; GO:0005515; F:protein binding; IEA:InterPro.

```
RA
     Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA
     Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA
     Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA
     Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
     Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA
RA
     Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA
     Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA
     Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
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     Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA
     Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA
     Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA
     Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA
     Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA
     Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA
     Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
     Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA
RA
     Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA
     Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA
     Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA
     Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA
     Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA
     Hayashizaki Y.;
RT
     "The transcriptional landscape of the mammalian genome.";
RL
     Science 309:1559-1563(2005).
RN
RP
     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC
     STRAIN=C57BL/6, and C57BL/6J; TISSUE=Brain, and Embryo;
RX
     PubMed=15489334; DOI=10.1101/gr.2596504;
RG
     The MGC Project Team;
RT
     "The status, quality, and expansion of the NIH full-length cDNA
RT
     project: the Mammalian Gene Collection (MGC).";
RL
     Genome Res. 14:2121-2127(2004).
CC
     -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC
          to dilysine motifs and reversibly associates with Golqi non-
CC
         clathrin-coated vesicles, which further mediate biosynthetic
CC
         protein transport from the ER, via the Golqi up to the trans Golqi
CC
         network. Coatomer complex is required for budding from Golgi
CC
         membranes, and is essential for the retrograde Golgi-to-ER
CC
         transport of dilysine-tagged proteins. In mammals, the coatomer
         can only be recruited by membranes associated to ADP-ribosylation
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 6 of 25

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,

Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,

Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,

Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,

Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,

di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,

Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,

Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,

Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

"Murine Copz1 gene encoding nonclathrin coat protein zeta-COP.";

Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.

Muroidea; Muridae; Murinae; Mus; Mus.

NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].

PubMed=16141072; DOI=10.1126/science.1112014;

Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,

NCBI_TaxID=10090;

STRAIN=C57BL/6J;

Hahn Y., Chung J.H.;

NUCLEOTIDE SEQUENCE [MRNA].

OC.

OX NCB RN [1] RP NUC

RA

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RN RP

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RA RA

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RA

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CC complex (By similarity).

CC -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,

CC beta, beta', gamma, delta, epsilon and zeta subunits (By

similarity).

CC -!- SUBCELULUAR LOCATION: Cytoolasm (By similarity), Golgi apparatus
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 7 of 25

-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus CC membrane; Peripheral membrane protein; Cytoplasmic side (By CC similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane; CC Peripheral membrane protein; Cytoplasmic side (By similarity). CC Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic CC side of the Golgi, as well as on the vesicles/buds originating CC from it (By similarity). CC -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By CC similarity). CC -!- SIMILARITY: Belongs to the adaptor complexes small subunit family. CC CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms CC Distributed under the Creative Commons Attribution-NoDerivs License

factors (ARFs), which are small GTP-binding proteins; the complex

processing, activity, and endocytic recycling of LDL receptors (By

also influences the Golgi structural integrity, as well as the

-!- FUNCTION: The zeta subunit may be involved in regulating the coat

assembly and, hence, the rate of biosynthetic protein transport

due to its association-dissociation properties with the coatomer

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DR EMBL; AK003302; BAB22703.1; -; mRNA.
DR EMBL; BC002246; -; NOT_ANNOTATED_COS; mRNA.
DR EMBL; BC058524; AAH58524.1; -; mRNA.
DR EMBL; BC083314; AAH83314.1; -; mRNA.

DR IPI; IPI00139637; -.
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DR MGI; MGI:1929063; Copz1.
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CC

CC

CC

CC

CC

CC

similarity).

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DR HOVERGEN; HBG051077; -.

DR InParanoid; P61924; -.

DR OMA; YDDTYPT; -.

DR PhylomeDB; P61924; -.

DR NextBio; 312654; -.
DR ArrayExpress; P61924; -.
DR Bgee; P61924; -.

DR

PE

DR CleanEx; MM_COP21; -.

DR Genevestigator; P61924; -.

GermOnline; BNSWIGS0000060992; Mus musculus.

GG; GO:0030126; C:COPI vesicle coat; ISS:UniProtKB.

DR GO; GO:0005891; P:intra-Golgi vesicle-mediated transport; ISS:UniProtKB.

DR G0; G0:0006886; P:intracellular protein transport; IEA:InterPro.
DR InterPro; IPR022775; AP_mu_sigma_su.
DR InterPro; IPR000804; Clathrin_sm-chain_CS.
DR InterPro; IPR011012; Longin-like.

DR InterPro; IPR000804; Clathrin_sm-chair DR InterPro; IPR011012; Longin-like. DR Pfam; PF01217; Clat_adaptor_s; 1. DR SUPFAM; SSF64356; Longin like; 1.

> PROSITE; PS00989; CLAT_ADAPTOR_S; 1. 2: Evidence at transcript level;

http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11

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 Matches 177; Conservative
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GN Name=COPZ1; Synonyms=COPZ;
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    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC 
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OC.
    Catarrhini; Hominidae; Pongo.
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RC
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    The German cDNA consortium;
RL
    Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC
    -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC
        to dilysine motifs and reversibly associates with Golgi non-
CC
        clathrin-coated vesicles, which further mediate biosynthetic
CC
        protein transport from the ER, via the Golgi up to the trans Golgi
CC
        network. Coatomer complex is required for budding from Golgi
CC
        membranes, and is essential for the retrograde Golgi-to-ER
CC
        transport of dilysine-tagged proteins. In mammals, the coatomer
CC
        can only be recruited by membranes associated to ADP-ribosylation
CC
        factors (ARFs), which are small GTP-binding proteins; the complex
CC
        also influences the Golgi structural integrity, as well as the
CC
        processing, activity, and endocytic recycling of LDL receptors (By
CC
        similarity).
```

-!- FUNCTION: The zeta subunit may be involved in regulating the coat

-!- SUBUNIT: Oligomeric complex that consists of at least the alpha,

-!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus

http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010...

beta, beta', gamma, delta, epsilon and zeta subunits (By

assembly and, hence, the rate of biosynthetic protein transport

due to its association-dissociation properties with the coatomer

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 8 of 25

N-acetylmethionine (By similarity).

Phosphoserine (By similarity).

Coatomer subunit zeta-1.

100.0%; Score 882; DB 1; Length 177;

/FTId=PRO_0000193826.

Acetylation; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport;

Golgi apparatus; Membrane; Phosphoprotein; Protein transport;

SEQUENCE 177 AA; 20198 MW; 355530D032D3A049 CRC64;

1

161 161

KW

KW

FT CHAIN

FT

FT

FT MOD RES

SO

CC

CC

CC

CC

CC

CC

CC

complex (By similarity).

similarity).

Transport.

MOD RES

Query Match

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DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE
    2: Evidence at transcript level;
KW
    Acetylation; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport;
KW Golgi apparatus; Membrane; Phosphoprotein; Protein transport;
KW
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FT
                  1 177 Coatomer subunit zeta-1.
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FT
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FT MOD_RES 161 161 Phosphoserine (By similarity).
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  Matches 177; Conservative 0; Mismatches 0; Indels 0; Gaps
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-5... Page 9 of 25

membrane; Peripheral membrane protein; Cvtoplasmic side (Bv

similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;

Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic

Peripheral membrane protein; Cytoplasmic side (By similarity).

side of the Golgi, as well as on the vesicles/buds originating

-!- SIMILARITY: Belongs to the adaptor complexes small subunit family.

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-!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By

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DR GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; ISS:UniProtKB. DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.

CC

DR

DR

DR

from it (Bv similarity).

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DR UniGene; Pab.18608; -.

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SMR; Q5R5F2; 1-149.

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DR CTD; 100174699; -.

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DR InterPro; IPRO0804; Clathrin_sm-chain_CS.

DR InterPro; IPRO11012; Longin-like.

DR Pfam; PF01217; Clat_adaptor_s; 1.

DR SUPFAM; SSF64356; Lonqin_like; 1.

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DR GO; GO:0005515; F:protein binding; IEA:InterPro.

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OMA; YDDTYPT; -.

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RT
     "Genome sequence of the Brown Norway rat yields insights into
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RL
     Nature 428:493-521(2004).
RN
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RX
     PubMed=15632090; DOI=10.1101/gr.2889405;
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 10 of 25

SubName: Full=Coatomer protein complex, subunit zeta 1 (Predicted);

Eukarvota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,

Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,

Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,

Fosler C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,

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Name=Copz1; Synonyms=Copz1_predicted; ORFNames=rCG_50578;

02-NOV-2010, entry version 7.

Rattus norvegicus (Rat).

NCBI TaxID=10116;

STRAIN-Brown Norway;

IDENTIFICATION.

Ensembl:

SubName: Full=Uncharacterized protein;

Muroidea; Muridae; Murinae; Rattus.

Submitted (MAR-2010) to UniProtKB.

NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

PubMed=15057822; DOI=10.1038/nature02426;

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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 11 of 25
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Florea L., Di Francesco V., Miller J., Turner R., Yao A., Harris M.,

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Walenz B., Mobarry C., Merkulov G.V., Charlab R., Dew I., Deng Z.,
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     Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC
CC
    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC
    Distributed under the Creative Commons Attribution-NoDerivs License
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DR EMBL; CH474035; EDL86787.1; -; Genomic_DNA.
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DR RefSeq; NP_001101587.1; -.
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DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
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DR InterPro; IPR011012; Longin-like.
DR Pfam; PF01217; Clat_adaptor_s; 1.
DR SUPFAM; SSF64356; Longin_like; 1.
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 12 of 25
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Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
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RA
RA
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    Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA
    Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA
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RT
     "The transcriptional landscape of the mammalian genome.";
RL
     Science 309:1559-1563(2005).
RN
RP
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RC
     STRAIN=Mixed;
    MEDLINE=22036378; PubMed=12040188; DOI=10.1126/science.1069193;
RX
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    Mural R.J., Adams M.D., Myers E.W., Smith H.O., Miklos G.L., Wides R.,
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RA
     Kodira C.D., Lu F., Chen L., Deng Z., Evangelista C.C., Gan W.,
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Heiman T.J., Li J., Li Z., Merkulov G.V., Milshina N.V., Naik A.K.,

Kravitz S.A., Miller J.R., Mobarry C.M., Reinert K., Remington K.A.,

Guan P., Ji R.R., Gu Z., Wang Z.Y., Zhong F., Xiao C., Chiang C.C.,

Yandell M., Wortman J.R., Amanatides P.G., Hladun S.L., Pratts E.C.,

Zhang Q., Zheng X.H., Nusskern D.R., Lai Z., Lei Y., Zhong W., Yao A.,

Yooseph S., Zhao Q., Zheng L., Zhu S.C., Biddick K., Bolanos R.,

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    Nuri Z., Parker K.A., Prudhomme A.C., Puri V.N., Qureshi H.,
    Raley J.C., Reardon M.S., Regier M.A., Rogers Y.H., Romblad D.L.,
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RA
    Sprague A.C., Stewart E., Strong R.V., Suh E., Sylvester K.,
RA
    Thomas R., Tint N.N., Tsonis C., Wang G., Wang G., Williams M.S.,
RA
    Williams S.M., Windsor S.M., Wolfe K., Wu M.M., Zaveri J.,
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 13 of 25

Chaturvedi K., Gabrielian A.E., Ke Z., Sun J., Subramanian G., RA Venter J.C., Pfannkoch C.M., Barnstead M., Stephenson L.D.; RA RT "A comparison of whole-genome shotgun-derived mouse chromosome 16 and RT the human genome."; RL Science 296:1661-1671(2002). RN RP NUCLEOTIDE SEQUENCE. RC STRAIN=Mixed; RA Mural R.J., Adams M.D., Myers E.W., Smith H.O., Venter J.C.; RL Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases. RN RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA]. STRAIN-Czech II; TISSUE-Mammary tumor metastatized to lung. Tumor RC RC arose spontaneously; RX PubMed=15489334; DOI=10.1101/gr.2596504; RG The MGC Project Team; RT "The status, quality, and expansion of the NIH full-length cDNA RT project: the Mammalian Gene Collection (MGC)."; RL Genome Res. 14:2121-2127(2004). CC CC CC Distributed under the Creative Commons Attribution-NoDerivs License CC DR

Johnson J.E., Dodson K.L., Woodford K.J., Evans C.A., Gropman B., Rusch D.B., Venter E., Wang M., Smith T.J., Houck J.T., Tompkins D.E., Haynes C., Jacob D., Chin S.H., Allen D.R., Dahlke C.E., Sanders R.,

Nodell M., Ali F., An H.J., Baldwin-Pitts D., Beeson K.Y., Cai S.,

Coyne M.D., Crowder M., Danaher S., Davenport L.B., Desilets R.,

Carnes M., Carver A., Caulk P.M., Center A., Chen Y.H., Cheng M.L.,

Li K., Liu X., Levitsky A.A., Majoros W.H., Chen Q., Xia A.C.,

Lopez J.R., Donnelly M.T., Newman M.H., Glodek A., Kraft C.L.,

RA RA

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RA

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RA

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DR

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DR

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    EMBL; BC110679; AAI10680.1; -; mRNA.
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    EMBL; AK156758; BAE33841.1; -; mRNA.
DR
    EMBL; AK167636; BAE39687.1; -; mRNA.
DR EMBL; AK168382; BAE40310.1; -; mRNA.
DR EMBL; AK168471; BAE40362.1; -; mRNA.
DR EMBL; CH466550; EDL03927.1; -; Genomic_DNA.
DR IPI; IPI00139637; -.
DR RefSeg; NP 062791.1; -.
DR UniGene; Mm.29473; -.
DR ProteinModelPortal; Q542M2; -.
DR SMR; Q542M2; 1-149.
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    STRING; Q542M2; -.
DR
    PRIDE; 0542M2; -.
DR
    Ensembl; ENSMUST00000100162; ENSMUSP00000097738; ENSMUSG00000060992.
DR GeneID; 56447; -.
DR KEGG; mmu:56447; -.
DR CTD; 56447; -.
DR MGI; MGI:1929063; Copz1.
DR HOVERGEN; HBG051077; -.
DR
    InParanoid; Q542M2; -.
DR
    OMA; YDDTYPT; -.
DR
   PhylomeDB; 0542M2; -.
    NextBio; 312654; -
    ArrayExpress; Q542M2; -.
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COPZ1_BOVIN
ID COPZ1 BOVIN
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                                               177 AA.
AC
    P35604; Q5EA44;
DT
     01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
     27-JUN-2006, sequence version 2.
DT
DT 05-OCT-2010, entry version 74.
DE RecName: Full=Coatomer subunit zeta-1;
DE AltName: Full=Zeta-1-coat protein;
DE
              Short=Zeta-1 COP;
GN Name=COPZ1; Synonyms=COPZ;
    Bos taurus (Bovine).
OS
0C
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
     Mammalia; Eutheria; Laurasiatheria; Cetartiodactvla; Ruminantia;
OC.
     Pecora; Bovidae; Bovinae; Bos.
OX
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RN
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RP
    146-160.
RC
    TISSUE=Liver:
RX
    MEDLINE=94103328; PubMed=8276893; DOI=10.1083/jcb.123.6.1727;
RA
    Kuge O., Hara-Kuge S., Orci L., Ravazzola M., Amherdt M., Tanigawa G.,
RA
     Wieland F.T., Rothman J.E.;
RT
     "Zeta-COP, a subunit of coatomer, is required for COP-coated vesicle
RT
     assembly.";
     J. Cell Biol. 123:1727-1734(1993).
RL
RN
RP
     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RY
     PubMed=16305752; DOI=10.1186/1471-2164-6-166;
RA
    Harhay G.P., Sonstegard T.S., Keele J.W., Heaton M.P., Clawson M.L.,
RA
     Snelling W.M., Wiedmann R.T., Van Tassell C.P., Smith T.P.L.;
RT
     "Characterization of 954 bovine full-CDS cDNA sequences.";
RI.
    BMC Genomics 6:166-166(2005).
RN
RP
     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC
     STRAIN=Crossbred X Angus; TISSUE=Ileum;
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010...
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 14 of 25

100.0%; Score 882; DB 2; Length 177;

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1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120 61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120

0; Indels

0; Mismatches

DR

DR

DR

DR

DR

DR

PE

Db

Qу

Db

Query Match

Baee; 0542M2; -.

Genevestigator; Q542M2; -.

DR InterPro; IPR022775; AP mu sigma su. DR InterPro: IPR000804; Clathrin sm-chain CS. DR InterPro; IPR011012; Longin-like. DR Pfam; PF01217; Clat_adaptor_s; 1.

SUPFAM; SSF64356; Longin_like; 1.

2: Evidence at transcript level;

Best Local Similarity 100.0%; Matches 177; Conservative

PROSITE; PS00989; CLAT_ADAPTOR_S; 1.

GO; GO:0030117; C:membrane coat; IEA:InterPro.

GO; GO:0005515; F:protein binding; IEA:InterPro. DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.

SQ SEQUENCE 177 AA; 20198 MW; 355530D032D3A049 CRC64;

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121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Qv
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RESULT 6
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 15 of 25

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RG
     NIH - Mammalian Gene Collection (MGC) project;
RL
     Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC
     -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC
        to dilysine motifs and reversibly associates with Golgi non-
CC
        clathrin-coated vesicles, which further mediate biosynthetic
CC
        protein transport from the ER, via the Golgi up to the trans Golgi
CC
        network. Coatomer complex is required for budding from Golgi
CC
       membranes, and is essential for the retrograde Golgi-to-ER
CC
        transport of dilysine-tagged proteins. In mammals, the coatomer
CC
        can only be recruited by membranes associated to ADP-ribosylation
CC
        factors (ARFs), which are small GTP-binding proteins; the complex
CC
        also influences the Golgi structural integrity, as well as the
CC
       processing, activity, and endocytic recycling of LDL receptors (By
CC
        similarity).
CC
     -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC
        assembly and, hence, the rate of biosynthetic protein transport
CC
        due to its association-dissociation properties with the coatomer
CC
        complex.
CC
     -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC
        beta, beta', gamma, delta, epsilon and zeta subunits.
CC
     -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golqi apparatus
CC
        membrane; Peripheral membrane protein; Cytoplasmic side (By
CC
        similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC
         Peripheral membrane protein; Cytoplasmic side (By similarity).
CC
        Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
CC
        side of the Golgi, as well as on the vesicles/buds originating
CC
        from it (By similarity).
CC
     -!- PTM: Phosphorvlated upon DNA damage, probably by ATM or ATR (By
CC
        similarity).
CC
     -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC
CC
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CC
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CC
DR
     EMBL; X75935; CAA53539.1; -; mRNA.
DR EMBL; BT020662; AAX08679.1; -; mRNA.
DR EMBL; BT020725; AAX08742.1; -; mRNA.
DR EMBL; BC102358; AAI02359.1; -; mRNA.
DR IPI; IPI00685319; -.
DR PIR; A49465; A49465.
DR RefSeq; NP_776707.2; -.
DR
    UniGene; Bt.43744; -.
   ProteinModelPortal; P35604; -.
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DR
    SMR; P35604; 1-149.
DR
    IntAct; P35604; 2.
DR
    STRING; P35604; -.
DR Ensembl; ENSBTAT00000007088; ENSBTAP00000007088; ENSBTAG0000005384.
DR GeneID; 281707; -.
DR KEGG; bta:281707; -.
DR CTD; 281707; -.
DR eggNOG; maNOG17869; -.
DR HOVERGEN; HBG051077; -.
DR InParanoid; P35604; -.
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DR OrthoDB; EOG969TD6; -.
DR
    PhylomeDB; P35604; -.
DR
    BioCyc; CATTLE: 281707-MONOMER; -.
DR
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DR
    GO; GO:0005515; F:protein binding; IEA:InterPro.
DR
    GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; IDA:UniProtKB.
DR
    GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR
    GO; GO:0006890; P:retrograde vesicle-mediated transport, Golg. . .; TAS:UniProtKB.
DR
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DR
    InterPro; IPR000804; Clathrin_sm-chain_CS.
DR
    InterPro; IPR011012; Longin-like.
DR
     Pfam; PF01217; Clat_adaptor_s; 1.
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DR

SUPFAM; SSF64356; Longin like; 1.

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    24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT
    24-MAY-2005, sequence version 1.
DT
DT 05-OCT-2010, entry version 31.
DE SubName: Full=Coatomer protein complex, subunit zeta 1 variant;
DE Flags: Fragment;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN
RP
    NUCLEOTIDE SEQUENCE.
RC
     TISSUE=Renal proximal tubule;
RX MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
RA Maruyama K., Sugano S.;
RT
     "Oligo-capping: a simple method to replace the cap structure of
RT
    eukaryotic mRNAs with oligoribonucleotides.";
RL Gene 138:171-174(1994).
RN [2]
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RC TISSUE=Renal proximal tubule;
RX
    MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
     Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Suqano S.;
RA
RT
     "Construction and characterization of a full length-enriched and a 5'-
RT
    end-enriched cDNA library.";
RL
    Gene 200:149-156(1997).
RN
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RA
    Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA
    Tanaka A., Yokovama S.;
RL
     Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
CC
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http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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N-acetylmethionine (By similarity).

Phosphoserine (By similarity).

E -> Q (in Ref. 1; CAA53539).

99.5%; Score 878; DB 1; Length 177;

1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60

1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60 61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMTVLNCLFDSLSOMLRKNVEKRALLENMEG 120 121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

/FTId=PRO 0000193824.

DR

PE

KW

KW

KW

FT FT

SQ

Db

Qy

QУ Db

FT MOD_RES

FT MOD_RES

FT CONFLICT

Query Match

PROSITE; PS00989; CLAT ADAPTOR S; 1.

161 161

Best Local Similarity 99.4%;

7 7

Acetylation; Cytoplasm; Cytoplasmic vesicle;

1

Direct protein sequencing; ER-Golgi transport; Golgi apparatus;

Matches 176; Conservative 0; Mismatches 1; Indels 0; Gaps

Membrane; Phosphoprotein; Protein transport; Transport. 1 177 Coatomer subunit zeta-1.

SEQUENCE 177 AA; 20228 MW; D410249532C8BAF8 CRC64;

1: Evidence at protein level;

```
RESULT 7
053FU3 HUMAN
ID Q53FU3_HUMAN
                 Unreviewed: 177 AA.
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Distributed under the Creative Commons Attribution-NoDerivs License
CC
DR EMBL; AK223188; BAD96908.1; -; mRNA.
DR IPI; IPI00032851; -.
DR UniGene; Hs.505652; -.
DR STRING; 053FU3; -.
DR Ensembl: ENST00000262061; ENSP00000262061; ENSG00000111481.
DR HGNC; HGNC: 2243; COPZ1.
DR HOVERGEN; HBG051077; -.
DR ArrayExpress; Q53FU3; -.
DR Bgee; Q53FU3; -.
DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR GO; GO:0005515; F:protein binding; IEA:InterPro.
DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR InterPro; IPR022775; AP_mu_sigma_su.
DR InterPro; IPR000804; Clathrin sm-chain CS.
DR InterPro; IPR011012; Longin-like.
DR Pfam; PF01217; Clat_adaptor_s; 1.
DR SUPFAM; SSF64356; Longin_like; 1.
DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE
    2: Evidence at transcript level;
FT NON_TER 1 1
SQ SEQUENCE 177 AA; 20267 MW; 5E2530D17696A10D CRC64;
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  Best Local Similarity 99.4%;
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           1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
Qy
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          61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLRQMLRKNVEKRALLENMEG 120
Db
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Qv
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RESULT 8
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                    Unreviewed; 177 AA.
AC
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DT 04-APR-2006, integrated into UniProtKB/TrEMBL.
DT 04-APR-2006, sequence version 1.
DT 05-OCT-2010, entry version 22.
DE SubName: Full=OTTXETP00000008162;
GN Name=copz1; ORFNames=TTpA002p21.1-001;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC.
    Xenopodinae; Xenopus; Silurana.
OX
    NCBI_TaxID=8364;
RN
    [11]
RP
    NUCLEOTIDE SEQUENCE.
RA Amaya E., Ashurst J.L., Bonfield J.K., Croning M.D.R., Chen C-K.,
RA Davies R.M., Francis M.D., Garrett N., Gilchrist M.J., Grafham D.V.,
RA McLaren S.R., Papalopulu N., Rogers J., Smith J.C., Taylor R.G.,
RA Voigt J., Zorn A.M.;
RL Submitted (OCT-2006) to the EMBL/GenBank/DDBJ databases.
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CC
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 17 of 25

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DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR GO; GO:0005515; F:protein binding; IEA:InterPro.
DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR
    InterPro; IPR022775; AP_mu_sigma_su.
DR
    InterPro; IPR000804; Clathrin_sm-chain_CS.
DR
    InterPro; IPR011012; Longin-like.
DR Pfam; PF01217; Clat_adaptor_s; 1.
DR SUPFAM; SSF64356; Longin_like; 1.
DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE 2: Evidence at transcript level;
SQ SEQUENCE 177 AA; 20202 MW; 4739F11DFDBBD25E CRC64;
                         96.0%; Score 847; DB 2; Length 177;
  Query Match
  Best Local Similarity 93.2%;
  Matches 165; Conservative 11; Mismatches 1; Indels 0; Gaps
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
Qv
Dh
            1 MDAILLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEQKAFEKNIFNKTHRTDSEIA 60
Οv
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMEG 120
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
QУ
          121 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 177
RESULT 9
A0AUT9_XENLA
                      Unreviewed;
ID AOAUT9_XENLA
                                            177 AA.
AC AOAUT9;
DT 28-NOV-2006, integrated into UniProtKB/TrEMBL.
DT 28-NOV-2006, sequence version 1.
DT 05-OCT-2010, entry version 17.
DE
   SubName: Full=Copz1 protein;
GN Name=Copz1;
OS
    Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC
    Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Embryo;
RG NIH - Xenopus Gene Collection (XGC) project;
RL
     Submitted (OCT-2006) to the EMBL/GenBank/DDBJ databases.
CC
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CC
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CC
DR EMBL; BC124924; AAI24925.1; -; mRNA.
DR UniGene; X1.76078; -.
DR ProteinModelPortal; A0AUT9; -.
DR SMR; A0AUT9; 1-149.
DR HOVERGEN; HBG051077; -.
DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR
     GO; GO:0005515; F:protein binding; IEA:InterPro.
DR
     GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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DR

DR

EMBL; CR760836; CAJ83159.1; -; mRNA.

UniGene; Str.5365; -. DR ProteinModelPortal; Q28HL1; -. DR SMR; Q28HL1; 1-149. DR STRING; Q28HL1; -DR HOVERGEN; HBG051077; -.

```
DR
    InterPro; IPR022775; AP_mu_sigma_su.
DR InterPro; IPR000804; Clathrin_sm-chain_CS.
DR InterPro; IPR011012; Longin-like.
DR Pfam; PF01217; Clat_adaptor_s; 1.
DR SUPFAM; SSF64356; Longin like; 1.
DR PROSITE: PS00989; CLAT ADAPTOR S: 1.
PE 2: Evidence at transcript level;
SQ SEQUENCE 177 AA; 20188 MW; 529B50DAF6D85058 CRC64;
  Query Match
                        95.9%; Score 846; DB 2; Length 177;
  Best Local Similarity 93.2%;
  Matches 165; Conservative 11; Mismatches 1; Indels 0; Gaps
           1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
Db
           1 MDAVLLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEOKAFEKNIFNKTHRTDSEIA 60
          61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Qv
Db
          61 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMEG 120
         121 LFLAVDEIVDGGVILESDPOOVVHRVALRGEDVPLTEOTVSOVLOSAKEOIKWSLLR 177
Qу
Db
         121 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 177
RESULT 10
0801P3 XENLA
ID Q801P3_XENLA
                      Unreviewed; 187 AA.
AC 0801P3;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 05-OCT-2010, entry version 29.
DE
    SubName: Full=Copz1 protein;
DE Flags: Fragment;
GN Name=Copz1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI_TaxID=8355;
RN
    [1]
RP
    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC
    TISSUE=Embryo;
RG NIH - Xenopus Gene Collection (XGC) project;
RL
    Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC
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CC -----
DR EMBL; BC047988; AAH47988.1; -; mRNA.
DR UniGene; X1.76078; -.
DR ProteinModelPortal; Q801P3; -.
DR HOVERGEN; HBG051077; -.
DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR GO; GO:0005515; F:protein binding; IEA:InterPro.
DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR InterPro; IPR022775; AP_mu_sigma_su.
DR InterPro; IPR000804; Clathrin_sm-chain_CS.
DR InterPro; IPR011012; Longin-like.
DR Pfam; PF01217; Clat_adaptor_s; 1.
DR SUPFAM; SSF64356; Longin_like; 1.
DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE
     2: Evidence at transcript level;
FT
    NON TER
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 19 of 25

DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.

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95.9%; Score 846; DB 2; Length 187;
  Best Local Similarity 93.2%;
  Matches 165; Conservative 11; Mismatches 1; Indels 0; Gaps 0;
           1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
Qy
Πh
          11 MDAVLLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEOKAFEKNIFNKTHRTDSEIA 70
Qv
          61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Db
           71 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMEG 130
         121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Qy
          131 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 187
Db
RESHLT 11
09IB48 DANRE
ID Q9IB48_DANRE
                           Unreviewed;
                                            177 AA.
AC
    09IB48;
    01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT
DT 01-OCT-2000, sequence version 1.
DT 05-OCT-2010, entry version 48.
DE SubName: Full=Nonclathrin coat protein zetal-COP;
GN Name=copz1;
OS Danio rerio (Zebrafish) (Brachydanio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX
    NCBI_TaxID=7955;
RN
    [1]
RP
    NUCLEOTIDE SEQUENCE.
RA Hahn Y., Chung J.H.;
RT "Identification of zeta-COP genes from various organisms.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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CC
DR EMBL; AB040044; BAA92783.1; -; mRNA.
DR
    IPI; IPI00489034; -.
DR
    RefSeq; NP_571583.1; -.
DR
    UniGene; Dr.79072; -.
DR ProteinModelPortal; Q9IB48; -.
DR SMR; Q9IB48; 1-149.
DR STRING; Q9IB48; -.
DR Ensembl; ENSDART00000011201; ENSDARP00000015008; ENSDARG00000017844.
DR GeneID; 57970; -.
DR KEGG; dre:57970; -.
DR NMPDR; fig|7955.3.peg.20733; -.
DR CTD; 57970; -.
DR ZFIN; ZDB-GENE-000406-6; copz1.
DR HOVERGEN; HBG051077; -.
DR
    InParanoid; Q9IB48; -.
DR OMA; YDDTYPT; -.
DR OrthoDB; EOG969TD6; -.
DR PhylomeDB; Q9IB48; -.
DR ArrayExpress; Q9IB48; -.
DR Bgee; 09IB48; -.
DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR GO; GO:0005515; F:protein binding; IEA:InterPro.
DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR
    GO; GO:0002088; P:lens development in camera-type eye; IMP:ZFIN.
DR
     GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 20 of 25

SO SEQUENCE 187 AA; 21167 MW; 7BC34FFA40CA56E4 CRC64;

Query Match

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QУ
          61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
              Πh
          61 LLEGLTVVYKSNIDLYFYVIGSSHENELMLMSVLNCLFDSLSQMLRKNVEKRALLENMEG 120
         121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Qv
Db
         121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177
RESULT 12
O6GOGO XENLA
ID Q6GQG0_XENLA
                     Unreviewed:
AC Q6GQG0;
DT 19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2004, sequence version 1.
DT 05-OCT-2010, entry version 33.
DE
    SubName: Full=MGC80093 protein;
GN
    Name=copz1; Synonyms=MGC80093;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
OX NCBI TaxID=8355;
RN
RP
    NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC
    TISSUE=Spleen;
RG NIH - Xenopus Gene Collection (XGC) project;
RL
     Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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CC
DR EMBL; BC072784; AAH72784.1; -; mRNA.
DR RefSeg; NP 001085450.1; -.
DR UniGene; X1.45820; -.
DR ProteinModelPortal; Q6GQG0; -.
DR SMR; Q6GQG0; 1-149.
DR
    GeneID; 443876; -.
DR
    KEGG; x1a:443876; -.
DR
    Xenbase; XB-GENE-6251726; copz1.
DR HOVERGEN; HBG051077; -.
DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR GO; GO:0005515; F:protein binding; IEA:InterPro.
DR
    GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR
    GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR
    InterPro; IPR022775; AP_mu_sigma_su.
DR
    InterPro; IPR000804; Clathrin_sm-chain_CS.
DR
    InterPro; IPR011012; Longin-like.
DR
     Pfam; PF01217; Clat_adaptor_s; 1.
DR
     SUPFAM; SSF64356; Longin like; 1.
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 21 of 25

95.8%; Score 845; DB 2; Length 177;

1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60

1 MDTLILEPSLYTVKAVLIMDNDGERLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Matches 165; Conservative 11; Mismatches 1; Indels 0; Gaps

InterPro; IPR022775; AP mu sigma su.

InterPro; IPR011012; Longin-like. DR Pfam; PF01217; Clat_adaptor_s; 1. DR SUPFAM; SSF64356; Longin_like; 1. DR PROSITE; PS00989; CLAT ADAPTOR S; 1. PE 2: Evidence at transcript level:

Best Local Similarity 93.2%;

InterPro; IPR000804; Clathrin_sm-chain_CS.

SQ SEQUENCE 177 AA; 20279 MW; EC44BED1889FEA07 CRC64;

DR

DR

Db

Query Match

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1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
Db
           1 MDAVLLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEQKAFEKNIFNKTHRTDSEIA 60
          61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Qv
Dh
          61 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMDG 120
0v
         121 LFLAVDEIVDGGVILESDPOOVVHRVALRGEDVPLTEOTVSOVLOSAKEOIKWSLLR 177
             Db
         121 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 177
RESULT 13
07SXH1 DANRE
ID Q7SXH1_DANRE
                          Unreviewed: 177 AA.
AC Q7SXH1;
DT 01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2003, sequence version 1.
DT 05-OCT-2010, entry version 41.
DE SubName: Full=Coatomer protein complex, subunit zeta 1;
GN Name=copz1;
OS Danio rerio (Zebrafish) (Brachydanio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC TISSUE=Whole body;
RG NIH - Zebrafish Gene Collection (ZGC) project;
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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CC
DR EMBL; BC055604; AAH55604.1; -; mRNA.
DR
    IPI; IPI00489034; -.
DR UniGene; Dr.79072; -.
DR ProteinModelPortal; Q7SXH1; -.
DR SMR; Q7SXH1; 1-149.
DR STRING; Q7SXH1; -.
DR PRIDE; O7SXH1; -.
DR Ensembl; ENSDART00000011201; ENSDARP00000015008; ENSDARG00000017844.
DR ZFIN; ZDB-GENE-000406-6; copzl.
DR eggNOG; fiNOG12172; -.
DR HOGENOM; HBG326766; -.
DR HOVERGEN; HBG051077; -.
DR InParanoid; Q7SXH1; -.
DR PhylomeDB; Q7SXH1; -.
DR ArrayExpress; Q7SXH1; -.
DR Bgee; Q7SXH1; -.
DR GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR GO; GO:0005515; F:protein binding; IEA:InterPro.
DR GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR InterPro; IPR022775; AP_mu_sigma_su.
DR
     InterPro; IPR000804; Clathrin_sm-chain_CS.
DR
     InterPro; IPR011012; Longin-like.
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 22 of 25

95.6%; Score 843; DB 2; Length 177;

Matches 164; Conservative 12; Mismatches 1; Indels 0; Gaps 0;

PROSITE; PS00989; CLAT_ADAPTOR_S; 1. 2: Evidence at transcript level;

Best Local Similarity 92.7%;

Query Match

SQ SEQUENCE 177 AA; 20174 MW; 529B51DBF6D95158 CRC64;

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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 23 of 25
     Pfam; PF01217; Clat adaptor s; 1.
DR
     SUPFAM; SSF64356; Longin_like; 1.
DR PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE 2: Evidence at transcript level;
SQ SEQUENCE 177 AA; 20311 MW; BC44BEC188939BDC CRC64;
  Ouerv Match
                         95.5%; Score 842; DB 2; Length 177;
  Best Local Similarity 92.7%;
  Matches 164; Conservative 12; Mismatches 1; Indels
                                                             0; Gaps
            1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
Db
            1 MDTLILEPSLYTVKAVLIMDNDGERLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSOMLRKNVEKRALLENMEG 120
Db
           61 LLEGLTVMYKSNIDLYFYVIGSSHENELMLMSVLNCLFDSLSOMLRKNVEKRALLENMEG 120
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
Qу
Db
          121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177
RESULT 14
C3KJY4_ANOFI
ID C3KJY4_ANOFI
                           Unreviewed; 177 AA.
AC C3KJY4;
DT 16-JUN-2009, integrated into UniProtKB/TrEMBL.
DT 16-JUN-2009, sequence version 1.
DT 05-OCT-2010, entry version 8.
DE SubName: Full=Coatomer subunit zeta-1;
GN Name=COPZ1;
OS Anoplopoma fimbria (Sablefish).
OC.
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC.
    Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Anoplopomatoidei; Anoplopomatidae; Anoplopoma.
OX NCBI_TaxID=229290;
RN
RP
    NUCLEOTIDE SEQUENCE.
RC
    TISSUE=Brain:
RA
    Messmer A., Rondeau E., Sanderson D., Cooper G., Leong J., Koop B.F.;
RT
    "Anoplopoma fimbria ESTs and full-length cDNAs.";
RL
     Submitted (MAY-2009) to the EMBL/GenBank/DDBJ databases.
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CC
DR EMBL; BT083249; ACQ58956.1; -; mRNA.
DR GO; GO:0006810; P:transport; IEA:InterPro.
DR InterPro; IPR022775; AP_mu_sigma_su.
DR InterPro; IPR011012; Longin-like.
DR Pfam; PF01217; Clat_adaptor_s; 1.
    SUPFAM; SSF64356; Longin_like; 1.
DR
PE
     2: Evidence at transcript level;
SO
     SEQUENCE 177 AA; 20187 MW; E665075A8B25F591 CRC64;
  Query Match
                         94.8%; Score 836; DB 2; Length 177;
  Best Local Similarity 92.7%;
  Matches 164; Conservative 12; Mismatches 1; Indels 0; Gaps
           1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEOKAFEKNIFNKTHRTDSEIA 60
Qу
           1 MDSPILEPSLHTVKAVLILDNDGDRLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60
Db
           61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
Qv
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http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11

```
RA Davidson W.S., Koop B.F.;
RT
    "Salmo salar and Esox lucius full-length cDNA seguences reveal changes
RT in evolutionary pressures on a post-tetraploidization genome.";
RL BMC Genomics 11:279-279(2010).
RN
     [2]
RP
    NUCLEOTIDE SEQUENCE.
RC
    TISSUE=Brain;
    cGRASP (B.F. Koop & W.S. Davidson);
RG
RA Leong J., von Schalburg K., Cooper G., Moore R., Holt R.,
RA Davidson W.S., Koop B.F.;
RL Submitted (OCT-2008) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG cGRASP (B.F. Koop & W.S. Davidson);
RT.
     Submitted (AUG-2010) to the EMBL/GenBank/DDBJ databases.
RN
     [4]
RP
    NUCLEOTIDE SEQUENCE.
RC
     TISSUE=Mixed brain:
RG cGRASP (B.F. Koop & W.S. Davidson);
RA Leong J., von Schalburg K., Cooper G., Moore R., Holt R.,
RA Davidson W.S., Koop B.F.;
RT
     "Salmo salar full-length cDNAs.";
RL Submitted (FEB-2009) to the EMBL/GenBank/DDBJ databases.
RN [5]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG
    cGRASP (B.F. Koop & W.S. Davidson);
RA
     Leong J., von Schalburg K., Cooper G., Moore R., Holt R.,
RA
    Davidson W.S., Koop B.F.;
RL
    Submitted (FEB-2009) to the EMBL/GenBank/DDBJ databases.
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DR EMBL; BT046324; ACI66125.1; -; mRNA.
DR EMBL; BT058392; ACN10105.1; -; mRNA.
DR EMBL; BT060094; ACN12454.1; -; mRNA.
DR
     HOVERGEN; HBG051077; -.
DR
     GO; GO:0030117; C:membrane coat; IEA:InterPro.
http://es/ScoreAccessWeb/GetItem.action?AppId=09556178&seqId=09323b6780fb2279&ItemName=2010... 1/10/11
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 24 of 25

61 LLEGLTVVYKSNIDLFFYVIGSSHENELMLMAVLNCLFDSLSOMLRKNVERRALLENMEG 120

121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177

121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177

Unreviewed; 177 AA.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmoninae; Salmo.

25-NOV-2008, integrated into UniProtKB/TrEMBL.

RX PubMed=20433749; DOI=10.1186/1471-2164-11-279; RA Leong J.S., Jantzen S.G., von Schalburg K.R., Cooper G.A., RA Messmer A.M., Liao N.Y., Munro S., Moore R., Holt R.A., Jones S.J.,

25-NOV-2008, sequence version 1. DT 02-NOV-2010, entry version 10. DE SubName: Full=Coatomer subunit zeta-1;

OS Salmo salar (Atlantic salmon).

Db

Qv

Db

DT

RN RP

RC

RESULT 15 B5X5K5 SALSA ID B5X5K5_SALSA

AC B5X5K5; DT

GN Name=COPZ1;

OX NCBI_TaxID=8030;

TISSUE=Brain:

NUCLEOTIDE SEQUENCE.

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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09... Page 25 of 25
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     GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR
DR
     InterPro; IPR022775; AP mu sigma su.
     InterPro; IPR000804; Clathrin_sm-chain_CS.
DR
DR
     InterPro; IPR011012; Longin-like.
     Pfam; PF01217; Clat_adaptor_s; 1.
DR
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-5... Page 1 of 12

SCORE Search Results Details for Application 09556178 and Search Result 20101214 103256 us-09-556-178-5.rapbm.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214 103256 us-09-556-178-5.rapbm.

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GenCore version 6.3 Copyright (c) 1993 - 2010 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2010, 11:27:17; Search time 143 Seconds

(without alignments)

1680.685 Million cell updates/sec

Title: US-09-556-178-5

Perfect score: 882

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Scoring table: BLOSUM62

Searched:

Gapop 10.0 , Gapext 0.5

6210261 segs, 1354514112 residues

Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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8: /ABSS/Data/CRF/ptodata/1/pubpaa/US12_PUBCOMB.pep:* SUMMARIES

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882 100.0 177 5 US-10-528-143-26 Sequence 26, App. 882 100.0 177 6 US-11-311-334-73107 Sequence 73107, 822 100.0 177 6 US-11-443-428A-819809 Sequence 819809, 882 100.0 177 7 US-11-597-825-1351 Sequence 819809, 882 100.0 177 8 US-12-399-906-29 Sequence 299, App. 882 100.0 192 6 US-11-443-428A-819804 Sequence 819804, 882 100.0 192 6 US-11-443-428A-819805 Sequence 819806, 882 100.0 192 6 US-11-443-428A-819806 Sequence 819808, Sequence 73107, A Sequence 1351, Ap Sequence 29, Appl

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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-5 Page 2 of 12								
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44	440	49.9		3		Sequence 776, App		
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125 6 US-11-443-428A-819817 ALIGNMENTS

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; Publication No. US20050226879A1
; GENERAL INFORMATION:
; APPLICANT: Ullman, Katharine
; APPLICANT: Liu, Jin
; APPLICANT: Prunuske, Amy
; APPLICANT: Dimaano, Christian
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATED TO
; TITLE OF INVENTION: INHIBITING NUCLEAR ENVELOPE BREAKDOWN
  FILE REFERENCE: 21101.0045U2
  CURRENT APPLICATION NUMBER: US/10/528,183
  CURRENT FILING DATE: 2005-03-17
  PRIOR APPLICATION NUMBER: PCT/US03/29267
  PRIOR FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: 60/411,248
; PRIOR FILING DATE: 2002-09-17
; NUMBER OF SEQ ID NOS: 35
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; SEO ID NO 26
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   ORGANISM: Artificial Sequence
   FEATURE:
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; Sequence 73107, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
; APPLICANT: CARRINO, JOHN
  APPLICANT: LIANG, FENG
   TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
  TITLE OF INVENTION: IDENTIFYING MATCHED REAGENTS
   FILE REFERENCE: INV-1005-UT2
   CURRENT APPLICATION NUMBER: US/11/371,354
   CURRENT FILING DATE: 2006-03-07
   PRIOR APPLICATION NUMBER: 60/673,045
   PRIOR FILING DATE: 2005-04-19
   PRIOR APPLICATION NUMBER: 60/665,199
   PRIOR FILING DATE: 2005-03-25
  PRIOR APPLICATION NUMBER: 60/665,200
  PRIOR FILING DATE: 2005-03-25
  PRIOR APPLICATION NUMBER: 60/659,493
  PRIOR FILING DATE: 2005-03-07
  PRIOR APPLICATION NUMBER: 60/659,492
  PRIOR FILING DATE: 2005-03-07
   PRIOR APPLICATION NUMBER: 60/953,586
   PRIOR FILING DATE: 2005-02-15
   PRIOR APPLICATION NUMBER: 60/651,390
   PRIOR FILING DATE: 2005-02-08
; NUMBER OF SEQ ID NOS: 78682
; SOFTWARE: PatentIn version 3.3
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-5... Page 3 of 12

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0; Mismatches

OTHER INFORMATION: synthetic construct

Best Local Similarity 100.0%; Matches 177; Conservative

US-10-528-183-26 Ouerv Match

Qу

; APPLICANT: Azar, Idit ; APPLICANT: Bernstein, Jeanne ; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES ; FILE REFERENCE: 02/23929

; CURRENT APPLICATION NUMBER: US/11/443,428A

; CURRENT FILING DATE: 2006-05-31

; NUMBER OF SEQ ID NOS: 1034312 ; SOFTWARE: PatentIn version 3.1 ; SEQ ID NO 819809

; LENGTH: 177 ; TYPE: PRT ; ORGANISM: Homo sapiens

US-11-443-428A-819809

Db

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; Sequence 1351, Application US/11597825
; Publication No. US20090297536A1
; GENERAL INFORMATION:
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; APPLICANT: CHIN, Lynda ; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR

; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF ; TITLE OF INVENTION: CANCER ; FILE REFERENCE: DFN-059-2

; CURRENT APPLICATION NUMBER: US/11/597,825 ; CURRENT FILING DATE: 2006-11-27

; NUMBER OF SEQ ID NOS: 1528

; SOFTWARE: FastSEQ for Windows Version 4.0 ; SEQ ID NO 1351 $\,$

; LENGTH: 177 ; TYPE: PRT

; ORGANISM: Homo sapiens

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US-12-399-906-29
; Sequence 29, Application US/12399906
; Publication No. US20100226856A1
: GENERAL INFORMATION
; APPLICANT: Vitaliano, Franco
; APPLICANT: Vitaliano, Gordana D
; TITLE OF INVENTION: DYNAMIC BIO-NANOPARTICLE ELEMENTS
; FILE REFERENCE: FV3011
; CURRENT APPLICATION NUMBER: US/12/399,906
; CURRENT FILING DATE: 2009-09-23
; NUMBER OF SEQ ID NOS: 30
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; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
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; DATABASE ENTRY DATE: 2009-05-05
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; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanging
; APPLICANT: Dahari, Dvir
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-5... Page 5 of 12

```
APPLICANT: Levanon, Erez
   APPLICANT: Freilich, Shiri
  APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
  APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
   CURRENT APPLICATION NUMBER: US/11/443,428A
   CURRENT FILING DATE: 2006-05-31
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QУ
Dh
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; Sequence 819805, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
  APPLICANT: Mintz, Liat
   APPLICANT: Xie, Hanqing
   APPLICANT: Dahari, Dvir
   APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-5... Page 6 of 12

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; Publication No. US20070083334A1
; GENERAL INFORMATION:
  APPLICANT: Mintz, Liat
   APPLICANT: Xie, Hanqing
APPLICANT: Dahari, Dvir
   APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
  APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
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   CURRENT FILING DATE: 2006-05-31
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    ORGANISM: Homo sapiens
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  APPLICANT: Mintz, Liat
   APPLICANT: Xie, Hanging
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-5... Page 7 of 12

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APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
: APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
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; CURRENT FILING DATE: 2006-05-31
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; APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanqing
APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-5... Page 8 of 12

APPLICANT: Dahari, Dvir

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APPLICANT: Xie, Hanqing
   APPLICANT: Dahari, Dvir
  APPLICANT: Levanon, Erez
  APPLICANT: Freilich, Shiri
  APPLICANT: Beck, Nili
  APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
   APPLICANT: Hermesh, Chen
   APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09... Page 10 of 12
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   APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
   CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
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   APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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   APPLICANT: Xie, Hanqing
  APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
 ; APPLICANT: Freilich, Shiri
  APPLICANT: Beck, Nili
  APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
   APPLICANT: Hermesh, Chen
   APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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  APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanging
  APPLICANT: Dahari, Dvir
   APPLICANT: Levanon, Erez
  APPLICANT: Freilich, Shiri
  APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
: APPLICANT: Bernstein, Jeanne
; TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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December 14, 2010, 11:24:20 ; Search time 25 Seconds Run on:

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  GENERAL INFORMATION:
    APPLICANT: Bandman, Olga
    APPLICANT: Lal, Preeti
    APPLICANT: Guegler, Karl J.
    APPLICANT: Shah, Purvi
    APPLICANT: Corlev, Neil C.
    TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
   NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS:
     ADDRESSEE: Incyte Pharmaceuticals, Inc.
      STREET: 3174 Porter Dr.
      CITY: Palo Alto
      STATE: CA
      COUNTRY: USA
      ZIP: 94304
    COMPUTER READABLE FORM:
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      COMPUTER: IBM Compatible
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     NAME: Cerrone, Michael C.
      REGISTRATION NUMBER: 39,132
      REFERENCE/DOCKET NUMBER: PF-0417 US
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: 650-855-0555
      TELEFAX: 650-845-4166
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    APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Guegler, Karl J.
   APPLICANT: Shah, Purvi
   APPLICANT: Corley, Neil C.
    TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
   NUMBER OF SEQUENCES: 9
   CORRESPONDENCE ADDRESS:
     ADDRESSEE: Incyte Pharmaceuticals, Inc.
      STREET: 3174 Porter Dr.
      CITY: Palo Alto
      STATE: CA
      COUNTRY: USA
       ZIP: 94304
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      REFERENCE/DOCKET NUMBER: PF-0417 US
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      TELEPHONE: 650-855-0555
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; Sequence 819809, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanging
  APPLICANT: Dahari, Dvir
APPLICANT: Levanon, Erez
APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
   CURRENT APPLICATION NUMBER: US/11/443,428A
   CURRENT FILING DATE: 2006-05-31
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; Sequence 819804, Application US/11443428A
: Patent No. 7745391
; GENERAL INFORMATION:
  APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanging
  APPLICANT: Dahari, Dvir
  APPLICANT: Levanon, Erez
  APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
  APPLICANT: Bernstein, Jeanne
  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
  FILE REFERENCE: 02/23929
  CURRENT APPLICATION NUMBER: US/11/443,428A
  CURRENT FILING DATE: 2006-05-31
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; Sequence 819805, Application US/11443428;
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
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APPLICANT: Levanon, Erez
   APPLICANT: Freilich, Shiri
  APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
 ; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
  APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
   CURRENT APPLICATION NUMBER: US/11/443,428A
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; Patent No. 7745391
; GENERAL INFORMATION:
  APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanqing
APPLICANT: Dahari, Dvir
   APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
   CURRENT APPLICATION NUMBER: US/11/443,428A
   CURRENT FILING DATE: 2006-05-31
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; Patent No. 7745391
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  APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanqing
APPLICANT: Dahari, Dvir
  APPLICANT: Levanon, Erez
  APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
  APPLICANT: Bernstein, Jeanne
  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
  FILE REFERENCE: 02/23929
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; GENERAL INFORMATION:
  APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanging
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; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
: APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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; APPLICANT: Mintz, Liat
  APPLICANT: Xie, Hanqing
APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
; APPLICANT: Azar, Idit
; APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
  CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103255_us-09-5... Page 8 of 13

APPLICANT: Dahari, Dvir APPLICANT: Levanon, Erez

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   APPLICANT: Mintz, Liat
   APPLICANT: Xie, Hanqing
   APPLICANT: Dahari, Dvir
  APPLICANT: Levanon, Erez
  APPLICANT: Freilich, Shiri
  APPLICANT: Beck, Nili
  APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
   APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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   APPLICANT: Mintz, Liat
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Best Local Similarity 100.0%;

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Matches 177: Conservative 0: Mismatches

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   APPLICANT: Xie, Hanqing
   APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
 ; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
   CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
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    ORGANISM: Homo sapiens
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  Best Local Similarity
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; GENERAL INFORMATION:
  APPLICANT: Mintz, Liat
   APPLICANT: Xie, Hanging
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
   FILE REFERENCE: 02/23929
  CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
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; SEO ID NO 819821
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   ORGANISM: Homo sapiens
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; GENERAL INFORMATION:
   APPLICANT: Mintz, Liat
   APPLICANT: Xie, Hanqing
  APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
  APPLICANT: Freilich, Shiri
  APPLICANT: Beck, Nili
  APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
   APPLICANT: Hermesh, Chen
   APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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; GENERAL INFORMATION:
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; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
: APPLICANT: Zhu, Wei-Yong
; APPLICANT: Wasserman, Alon
; APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
   APPLICANT: Bernstein, Jeanne
   TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
  FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
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; Sequence 819807, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
; APPLICANT: Xie, Hanqing
; APPLICANT: Dahari, Dvir
; APPLICANT: Levanon, Erez
; APPLICANT: Freilich, Shiri
; APPLICANT: Beck, Nili
; APPLICANT: Zhu, Wei-Yong
  APPLICANT: Wasserman, Alon
  APPLICANT: Hermesh, Chen
  APPLICANT: Azar, Idit
APPLICANT: Bernstein, Jeanne
  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
; FILE REFERENCE: 02/23929
; CURRENT APPLICATION NUMBER: US/11/443,428A
; CURRENT FILING DATE: 2006-05-31
; NUMBER OF SEQ ID NOS: 1034312
; SOFTWARE: PatentIn version 3.1
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103255_us-09... Page 12 of 13

; APPLICANT: Mintz, Liat ; APPLICANT: Xie, Hanqing ; APPLICANT: Dahari, Dvir

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SCORE 3 0

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103255_us-09... Page 13 of 13

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103257_us-09-5... Page 1 of 12

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103257_us-09-556-178-5.rapbn.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214 103257 us-09-556-178-5.rapbn.

Go Back to previous page

GenCore version 6.3 Copyright (c) 1993 - 2010 Biocceleration Ltd.

OM protein - protein search, using sw model

Run on: December 14, 2010, 11:32:21 ; Search time 1 Seconds

(without alignments)

1087.643 Million cell updates/sec

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; FILE REFERENCE: PP022930.0003
; CURRENT APPLICATION NUMBER: US/12/800,898
; CURRENT FILING DATE: 2010-05-25
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; PRIOR FILING DATE: 2006-11-14
; PRIOR APPLICATION NUMBER: GB-0410866.8
; PRIOR FILING DATE: 2004-05-14
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TITLE OF INVENTION: POLYPEPTIDES FROM NON-TYPEABLE HAEMOPHILUS INFLUENZAE

RESULT 1 US-12-800-898-1740

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; Sequence 1740, Application US/12800898 ; Publication No. US20100303822A1 ; GENERAL INFORMATION: ; APPLICANT: MASIGNANI, Vega ; APPLICANT: ARICO, Maria

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